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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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JOURNAL COMMENT REFERENCE AUTHORS KEYWORDS. SOURCE ORGANISM RESULT 1 AL551859 LOCUS ACCESSION VERSION FEATURES DEFINITION source Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers Full-length cDNA libraries and normalization Unpublished (2001) AL551859 AL551859.1 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AL551859 AL551859 LTI_NFL006_PL2 prime, mRNA sequence /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="CSODIO61xJ24"
/clone_lib="LTI_NFLO06_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; S GI:12890210 te="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand primed with a NotI-ollgo(dT) primer. Five prime 982 bp mRNA linear EST 16-FEB-2001 Homo sapiens cDNA clone CS0DI061YJ24 5 end

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria;
1 (bases 1 to 814)
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6;
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/db_xref="taxon:9606"
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Seq primer: M1
POLYA=Yes:
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                                                                                                                                                                                                                                                                                                                                                                               Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of
CDNA Library Arrayed by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Resea
                                                                                                                                                                                                                                                                                                                                                                    Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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   /dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/lote="Organ: Lung; Vector: pT/T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EocR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
                                                                                                                                                                          /tissue_type="Primary
Cells"
                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-ENI-acv-k-12-0-UI"
/clone_11b="UI-CF-ENI"
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104 CCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAG
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National Institutes of Health, Mammalian
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                                     CAGGCCTCACCCAGCAACACAGTGTGGGAAGATCGCAAGTGACTGCCTTCCGCTTCCAGGAC
                                                                                                                                                         TCAGTGAAGTTTGAGGGGAACAAACAAACGGGACTTCAACCAGAACTTCATCCTGACCGCC
                                                                                                                                                                                                                                             CAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5589207"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host-"DH10B"
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90.9%;
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Pred. No. 9.7e-165;
O; Mismatches 63;
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M.
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, T
I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BF195575
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1 (bases 1 to 720)
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Location/Qualifiers
constructed by Bento Soares and M. 170 \text{ c} 169 \text{ g} 175 \text{ t} 1
                                                                                 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                           went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Ov18"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3571173"
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                                                                                                                     sequence.
AW274482
Tumor Gene Index
Unpublished (1997)
                                                                                                                                       AW274482 631 bp mRNA linear ES7 xv30c09.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE: 8814640 3' similar to WP:Y71F9A_279.B CE22843 ;,
                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 631)
                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACACACCACGAGGAATAAGCGCGGGGGTTTGCTGTACCGGCCTGTACATGGGCACAGCAC
                                                                                                                                                                                                                     AGTAGAGACTCTGATTCTGGAAATTCTGACAAATAATTTAATAATACACATG
                                                                                                                                                                                                                                                                 CTCAAGGATGTGAGGAACACAAGTTCATTTCTGTTGCTGGAGACACTGCAGACTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAAC
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Pred. No. 1.
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                                                                                                                                                                                same function.
                                                   Craniată; Vertebrata;
Catarrhini; Hominidae,
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                     Anatomy
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                                                                                                                 620 AGTTCATTTCTGTTGCTGCAGACACACTGCAGACTCCACTGTGCCGAGGTTGAACTCTTT
                                                                                                                                                                                                                                             271
                                                                                                                                                                                                                                                            500 GACTGCTTCCAGGACTGGGCCAGCTAGTGGGGGGTGGCAGAGGTCTCTTTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740, TTTTCAAAGTAGTAAACTTTTCTATTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                   380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                           GACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGGTGGCAGAGGTCTCTTTGCTTC
                              ATTCAGCCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCAAGGATGTGAGGAACACA
                                                                                                                                                                                       ATTCAGCCCTAGCTCTGTAGAGAAATGCAAACCTCGAACTCTCAAGGATGTGAGGAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 7.3e-164;
0; Mismatches . 1;
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REFERENCE
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K-EST0069490 S22SNU16 Homo sapiens cDNA clone S22SNU16-1-G02 5',
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                                                                                                                                                                                                                                                                                       49 CCCCTGGTTCCCCAAGGCAGAGGAAATACCCTGGTGGAGCCCTCCTTCCATAGAACCAGA 108
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                                                                                                                                                                                                                                               27 CCCCTGGTTCCCCAAGGCAGAGGAAATACCCTGGTGGAGCCCTCCTTCCATAGAACCAGA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Contact: Kim.YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BM789812
BM789812.1 Gi:19138044
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Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: yongsung@mail.kribb.re.kr
Plate: 1 row: G column: 02
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
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TGTCAATGTCTACTACACCACCATGGATAAGCGGCGGGGGTTTGCTGTTCCCGCCTGTACAT 228
                                                                                     TGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACAT
                                                                                                                                                                    GATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTT
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                                                                                                                                                                                                                                                                                                                         75.1%; Score 623; DB 14; Length 649; Ilarity 100.0%; Pred. No. 4.4e-162; Conservative .0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRi; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
ob_xref="taxon:9606"
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line="SNU-16"
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/clone="IMAGE:6029745" /clone_lib="Human insulinoma" /tissue_type="insulinoma"

/db_xref="taxon:9606"

BASE CO

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179

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Query Match Best Local Matches

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Similarity

73.9%; ilarity 100.0%; Conservative (

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602280989F1 NIH_MGC_86 Homo sapiens
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                                                                                                                                                                                                                                                                    TTTCTATTTTCTACTTGCCCCAGTAGAGACTCTGATTCTGGAAATTCTGACAAATAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library.
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/note="Organ: pancreas; Vector: pBluescript SK-; Site_1: XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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TGGGCCAGCTAGTGGGGGTGGCAGAGGTCTCNTTTGCTTCATCAGCC--TACTCTGTAG
               TGGGCCAGCTAGTGGGGGTGGCAGAGGTCTC-TTTGCTTCATTCAGCCCTAGCTCTGTAG
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/lab_host="DH10B (phage-resitant)"
/note="Organ: bone; Vector: pcMV-SPORT6; Site_1: NotI;
/note="Sili; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_86"
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Contact: Robert Strausberg, Ph.D.
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin

Note: The constructed by Ling Hong in the laboratory of Gerald M. Rubin

Note: The construction of Gerald M. 
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                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL. http://image.llnl.gov
Plate: LLAM13228 row: d column: 05
                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                               High quality sequence start: 284 High quality sequence stop: 651.
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               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                        ocation/Qualifiers
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181 CAAATCAGCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACG
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BQ421087
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National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1125)
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informations of the consortium o
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Site_2: Sall; Cloned unidirectionally. Primer: Ol
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138 TGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATA 197
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLCM299 row: g column: 02
High quality sequence stop: 627.
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NIH-MGC http://mgc.nci.nih.gov/
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TCATTCAGCCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCAAGGATGTGAGGAACA 617
                                                   GTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGGTGGCAGAGGTCTCTTTGCT
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/tissue_type="adenocarcinoma"
/lab host="DHIOB (phage-resistant)"
/lab host="DHIOB (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Corgan: pancreas; Vector: poTB7; Site_1: XhoI;
/note="Corgan: pancreas; Vector: potential"
/ site_2: EcoRI; ChoI sites using the pirectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library construct by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Lif Technologies)."
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Technologies)."
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/clone="IMAGE:3623065"
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hutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.4e-153;
0; Mismatches 1;
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ДУ	Qy. Db	Query Ma	BASE COUNT	•		FEATURES sou			TITLE JOURN COMMENT	REFERENCE	VERSION KEYWORDS SOURCE ORGANI	LOCUS DEFINITION	RESÙLT 13 BE794429	Оy	р _О у	Db 04	Db
e. e	nes		TUNDO		*	RES source		-	TITLE JOURNAL MMENT	ENCE	RSION YWORDS URCE ORGANISM	ITION	T 13			•	
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FEATURES Source	·()		REFERENCE AUTHORS TITLE JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION	RESULT 14	ОУ	Db .	•	Qy Db		Db Qy	Db Q	Db (Db ··	o b	Qy
77 (0.	CDMA Library Preparation: M. Bento Soares, Ph.D. cDMA Library Arrayed by: Greg Lennon, Ph.D. ph.D. DMA Sequencing by: Washington University Genome Sequencing C Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov	pher Moskaluk,	Catarrhini; Hominidae; nih.gov/ncicgap. ncer Genome Anatomy Pro	90 Chordata;	70		698 GGAGTCCCTTTCCTGAATATATACTTGTT 726	638 CGGAGACACTGCAGACTCCACTGTGCCGAGGTTGAACTCTTTTTTGTTGCTCAAGTTCTA		520 CTGGGCCAGCTAGTGGGGG-TGGCAGAGGTCTCTTTGCTTCATTCAGCCCTAGCTCTGTA	60 57	400 ATCAGTGAAGTTTGAGGGGAACAACAACGAGGACTTCAACCAGAACTTCATCCTGACCGC	340 CCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGG 	77	317 CCTGTACATGGGCACAGCCAGCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATC 317 CCTGTACATGGGCACAGCAACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATC	257 TGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCG CCTGTACATGGGCACAGCCACCCTGGTCTGGAATGCAATGCTGTTTCAGGACAAGAATC	160 TGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTG

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/clone_lib="NCI_CGAP_Kidll"
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db_xref="taxon:9606"
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Query Match
Best Local Similarity
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Tissue Procurement: ATCC
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National Institutes of Health, 1
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the laboratory of Gerald M. Rubin by Ling Hong in the Ling Hong 
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ALIGNMENTS

AAAO8036 standard; cDNA; 830 BP. XX AC AAAO8036; XX AC AAAO8036; XX YX AC AAAO8036; XX 19-JUN-2000 (first entry) XX DIT 19-JUN-2000 (first entry) XX Human protein transport molecule; PTAM; diagnosis; cytostatic; XX Human; protein transport molecule; PTAM; diagnosis; cytostatic; XX Human; protein transport molecule; PTAM; diagnosis; cytostatic; XX Mantiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic; XX Mantiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic; XX Mantiallergic; antidiabetic; antilipaemic; antilipaemic; antirheumatic; osteopathic; XX Mantiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic; XX Mantiallergic; antidiabetic; antilipaemic; antilipaemic; antirheumatic; osteopathic; XX Mantiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic; XX Mantiallergic; antidiabetic; antilipaemic; antilipaemic; antirheumatic; osteopathic; X	AAAO	AAAO8O36
	ID	08036 standard; cDNA;
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	AC	AAA08036;
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	DŢ	19-JUN-2000 (first entry)
	XX	
	DΕ	Human protein transport molecule (PTAM) encoding cDNA SEQ ID NO:10.
	×	
	×Σ	Human; protein transport molecule; PTAM; diagnosis; cytostatic;
	ΚW	antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic;
	KΣ	antiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic;
	ΚW	dermatological; antianaemic; antipsoriatic; hepatotropic; antigout;
	Κ¥	antiinflammatory; antiHIV; protein transport regulator; cancer;
	ΚW	immune disorder; cell proliferative disorder; secretory disorder;
	XW	urticaria; allergy; abnormal vesicle trafficking; asthma;
Homo sapiens. WO200012703-A2. 09-MAR-2000. 26-AUG-1999; 27-AUG-1998; (INCY-) INCYTE	XW	autoimmune haemolytic anaemia; ss.
Homo sapiens. W0200012703-A2. 09-MAR-2000. 26-A0G-1999; 27-AUG-1998; (INCY-) INCYTE	XX	
WO200012703-A2. 09-MAR-2000. 26-AUG-1999; 27-AUG-1998; (INCY-) INCYTE	SO	Homo sapiens.
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Bandman O,

Yue H, Corley NC,

Guegler KJ;

Gorgone GA,

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regulate protein transport. FrAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased cexpression or activity of PTAM. PTAM polynucleotides are useful for conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the conditions associated with PTAM and include cell conditions as cancers, immune disorders, secretory conditions as concers, immune disorders, secretory conditions as a sancers, immune disorders, secretory contained the conditions associated with abnormal vesicle contained the sallergies, asthma, urticaria and autoimmune contained the conditions as a targeting or delivery mechanism for bringing pharmaceutical agents contained the conditions of the province of the conditions of pTAM related contained the conditions of the conditions of pTAM related contained the conditions of the province of the conditions are useful for generating hybridisation probes useful in mapping the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               naturally occurring genomic sequences.
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DB; AAY82318.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CAAGGCAGAGGAAATACCCTGGTGGAGGCCCTCCTTCCATAGAACCAGAGATGGCATCTGT
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                                                      CAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACAC
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AGTGTGGAAGATCGCAAGTGACTGCTŢCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGTG
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Pred. No. 2.9e-248;
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26-JUL-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding a novel secreted protein, Seq ID 394.
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24-FEB-2000;
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19-MAY-2000;
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17-MAR-2000;
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The invention relates to isolated nucleic acid molecules and their cc encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, cc rabbits, yoats, horses, cats, dogs, chickens or sheep. They cc are also used in diagnosing a pathological condition or susceptibility cc be used in alleviating symptoms associated with the disorders and in cc diagnostic immunoassays e.g. radioimmunoassays or enzyme linked cc include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. recordiac arrest, cerebrovascular disorders e.g. neoplasms of the breast or liver, cc disorders disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other cc disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to
              08-NOV-2000;
08-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives
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P-PSDB; AAU16228.
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2000US-0241221. 2000US-0241785. 2000US-0241786. 2000US-0241787.

2000US-0236369

and

2000US-0241808 2000US-0241809 2000US-024487 2000US-0244617 2000US-0246474 2000US-0246475 2000US-0246475 2000US-0246478

14-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

14-AUG-20

14-AUG-2000; 14-AUG-2000;

14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities for correct livid to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevent skin agi
transplantation,
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                                      TGATTCTGGAAATTCTGACAAATAATTTAATAATACACATG 830
                                                                                                                       GAGGAACACAAGTTCATTTCTGTTGTTGCGGAGACACTGCAGACTCCACTGTGCCGAGGT
                                                                                                                                     GAGGAACACAAGTTCATTTCTGTTGTTGTGGGAGACACTGCAGACTCCACTGTGCCGAGGT
                                                                                                                                                                                                                        GATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGTGGCAGAGGTC
                                                                                                                                                                                                                                                                  GGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACACAGTGTGGGAA
                                                                                                                                                                                                                                                                                                             CCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTTGAGGGGAACAACAACG
                                                                                                                                                                                                                                                                                                                                                                                            CATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTG
TGATTCTGGAAATTCTGACAAATAATTTAATAATACACATG 795
                                                                                                                                                                                                             GATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGGTGGCAGAGGTC
                                                                                                                                                                                                                                                       GGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAA
                                                                                                                                                                                                                                                                                               CATGGATAAGCGGCGTTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTG
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ion, for su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 761; DB 22;
Pred. No. le-226;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 864;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                       Th present invention relates to the isolation of novel cDNA sequences encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful in gene therapy. AAS57325-AAS58880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 246; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-2000; 2000US-191597P.
04-MAY-2000; 2000US-202024P.
05-MAY-2000; 2000US-202189P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New colon tumour proteins and related nucleic treatment, prevention, diagnosis and monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
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  301
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                                                                                                                                                                                                                                                                                                                                             al Similarity
317; Conserv
                                                                                                                                                                                                                                        GTTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTT
                                                                      CCTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCACCACCATGGATAAGCGGCGGC
                            TCATCCTGACCGCCCAGG
                                                                                                             GCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTG
                                                                                                                            GCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCAGACCACGGTCCTTG
TCATNCTGACCGCCCAGG
                                                      GTTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTT
                                                                                                                                                                                                                                                                                 CCTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                 318 BP; 76 A; 82 C; 83 G; 76 T; 1 other;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Χu J,
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                                                                                                                                                                                                                                                                                                                                                         38.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                         Score 317; DB 2
Pred. No. 2e-88;
0; Mismatches
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(first entry)

AAS58525;

AAS58525 standard;

CDNA; 318

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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cular mRNA species, almost all the 3'-criented cDNAs hybridise with specific mRNAs. Each librate constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene signature HUMGS04611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1235-1236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene signature;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reflects relative abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in for diagnosis of abnormal cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1993;
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121
                                                                                                                 610
                                                                                                                                                                                                  550 TCTTTGCTTCATTCAGCCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCAAGGATGT
                                                                                                                                                                                                                                                                          326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cloning; mapping;
                                                                                                                                                                                                                                                1 GATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGGTGGCAGAGGTC
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                   GAGGAACACAAGTTCATTTCTGTTGCGGAGACACTGCAGACTCCACTGTGCCGAGGT
                                                                                                            GAGGAACACAAGTTCATTTCTGTTGCTGCGGAGACACTGCAGACTCCACTGTGCCGAGGT
                                                                                                                                                        TCTTTGCTTCATTCAGCCCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCAAGGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                   359 BP; 85
                                                                                                                                                                                                                                                                                                                                        35.8%; Score 297.4; DB 16; llarity (94.2%) Pred. No. 2.7e-82; Conservative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              abnormal cell function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-JP01916:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          messenger RNA; mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                              A; 76 C; 75 G; 114 T; 9 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-biased library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3'-directed human cDNA library - e.g. function, by preparing cDNA that corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                           Indels
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Each library
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                         729
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RESULT
CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer, and an oligonucleotide comprementary CC to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC colligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13632 to AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to CC CAAB95893 represent human amino acid sequences; and AAH13632 to AAH13632
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Ishii S,
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH07014 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA clone (5'-primer) SEQ ID NO:3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID 3849;
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K,
(, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346
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Query Match
Best Local :
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                                                                                                                                                                                                                                           antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic; antiallergic; antidiabetic; antilipaemic; antirhematic; osteopathic; dermatological; antianaemic; antipsoriatic; hapatotropic; antigout; antiinflammatory; antiHIV; protein transport regulator; cancer; antiinflammatory; antiHIV; protein transport regulator; cancer; immune disorder; cell proliferative disorder; secretory disorder;
                                                                                                                                                                                                                                                                                                                                               Human protein transport molecule (PTAM) encoding cDNA SEQ ID NO:15
                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA08041
Tang YT, L
Gorgone GA,
                                                                                                                                                          WO200012703-A2
                                                                                                                                                                                                                 autoimmune haemolytic anaemia; ss
                                         (INCY-) INCYTE PHARM INC
                                                                       27-AUG-1998;
                                                                                                  26-AUG-1999;
                                                                                                                                                                                                                                urticaria; allergy; abnormal vesicle trafficking; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 ATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA; 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAANGGGCAAA 706
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                                                                                                                                                                                                                                                                                                                                                                               (first entry)
Baughn MR, Patterson
                                                                                                                                                                                                                                                                                                                       transport molecule; PTAM; diagnosis; cytostatic;
                                                                       9805-0098206
                                                                                                    99WO-US19616
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   Yue H,
erson C;
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                Corley
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                                                                                                                                                                                                                                                                                                            antiarteriosclerotic
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                Guegler KJ;
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Sequence

1146 BP;

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                                                                                                                                                                                                                                      preventing or treating a disorder associated with decreased or increased expression or activity of PTAM. PTAM. polynucleotides are useful for diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                    trafficking; such as allergies, asthma, urticaria and autoimmune haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules (PTAMS) given in AAY82317 to AAY82324. The PTAMS cytostatic, antiarthritic, antiasthmatic, immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 74; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        regulate protein transport. PTAM proteins and antagonists are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatotropic, antigout, antiinflammatory and antiHIV activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antirheumatic, osteopathic, dermatological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic, antiallergic, antidiabetic, antilipaemic
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                                                 occurring genomic sequences.
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331 A; 212 C; 228 G;
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       375 T; 0 other;
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Š B ρ 밁 Ş D. Ş 밁 Š 밁 В Query Match Best Local (Matches 114 CATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCA 173 282 AGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTT 234 222 162 474 GCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGT 462 414 AGGGGAACAACAGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCA 402 354 ATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG 294 al Similarity 326; Conserv 582 AAAGGGGCAAAAGTCCATTCTCATTTGGTC TTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATG ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA ATGTCTACTACACCACCATGGATAAGCGGCGCGTTTGCTGTCCCGCCTGTACATGGGCA CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA GGGGGTGGCAGAGGTCTCTTTGCTTCATTC ACANTACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTT Conservative 30.3%; 0 Score 251.6; D Pred. No. le-67 0; Mismatches 611 贸 124; 21; Indels Length 0; Gaps 281 233 221 581 473 401 341 293 521 461 413 353

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Best Local S
Matches 326
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                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of human NTF2 associated protein 16. The sequences can be used in the treatment of cancer and HIV infection, as well as other diseases. The present sequence is the coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 24-25(Disclosure); 32pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide-human NTF2 associated protein 16 and
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454
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                                                                                                                                294 TTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATG
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                                                                                                                                                                            214 ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA
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                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                 ATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTTCCCGCCTGTACATGGGCA
                                                                 ATGAAGCCACACAGACCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG
                                                                                                                                                                                                                                                                     CGTCTCTGGATTTTAAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA
                                                                                                       AGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTT
                                                                                                                                                                                                                                                                                                                                                                               2581 BP;
ATGGAAACAAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCA
                          AGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCA
                                                   AGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated protein 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "NFT2 associated protein 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                               791 A; 449 C; 452 G; 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry;
                                                                                                                                                                                                                                                                                                                                     30.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2581
                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                         Score 251.6; DB:
Pred. No. 1.7e-67
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; HIV infection;
                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                                                                                                                                                              Ή,
                                                                                                                                                                                                                                                                                                                          124;
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                     2581;
                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
                                                                                                                                                                                                                                                                                                                         Gaps
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513
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                  the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                  the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length-CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer se comprises: (a) an oligo-dT primer and an oligonucleotide compleme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH17938 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishii
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                                                                                                                                                                                                                                                                                                                                                                  the complementary strand of a polynucleotide which comprises one of 5602 nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574 AAAGGGGCAAAAGTCCATTCTCATTTGGTC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 ACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTT 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGGTGGCAGAGGTCTCTTTGCTTCATTC 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sogai T, Nishikawa
Sugiyama T, Wakame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID 17706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2537pp + CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO:17706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense therapy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito
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Otsuki
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T;
                                                                                                                                                                                                                                                                                                                                                                                                          complementary
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represent oligonucleotides, all of the present invention

of which are used

the exemplification

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RESULT 9
ABV24535
ID ABV2
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Query Match
Best Local :
                                                                                                                                                                                                                                                                                pharmacogenomic
                                                                                                                                                                                                                                                                                               Human; prostate
                                                                                                                                                                                                                                                                                                                      Human prostate expression marker
                                                                                                                                                                                                                                                                                                                                                   16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                             ABV24535
                                                                                                                                                                                                                                                                                                                                                                                                      ABV24535 standard; cDNA;
                                                                                                                                                                                                                               WO200160860-A2
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                 17-FEB-2000;
                                    Schlegel R,
                                                                                                                                                                           20-FEB-2001;
                                                                                                                                                                                                      23-AUG-2001
                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                            )9-JUN-2000;
                                                                                                                        25-MAY-2000;
                                                                                                                                      6-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 TTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 ATGTCTACTACACCACCATGGATAAGCGGCGCGTTTGCTGTCCCGCCTGTACATGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAGCCACACCAAGCCAGACCACGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2692 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGTGGCAGAGGTCTCTTTGCTTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGGGGCAAAAGTCCATTCTCATTTGGTC
                                                                                  2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2119007P.
2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                    Endege
                                                                                                                                                                            2001WO-US05171
                                                                                                                                                                                                                                                                                  cancer; cytostatic; carcinogen;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                        2994
                                      Monahan JE;
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Pred. No. 1.7e-67;
0; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 G; 890 T; 0 other;
                                                                                                                                                                                                                                                                                                                            CDNA 24526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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RESULT 10 AAS26214 ID AAS26

AAS26214 standard;

cDNA;

1387

AAS26214;

Human cDNA 07-NOV-2001

encoding a novel

secreted protein,

Seq ID 393.

nootropic;

(first entry)

Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootro

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Best Local Similarity
Matches 326; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for: specification or patient is affilicted with prostate cancer; (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usel for detecting presence of prostate cancer, stage of prostate cancer % \left( 1\right) =1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e) selecting a composition for inhibiting prostate cancer in a patient;(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 CATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 ATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
                                                                                                        474
                                                                                                                                           416
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                                                                                                        GCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGT
                                                                                                                                           ATGGAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCA
                                                                                                                                                             AGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCA
                                                                                                                                                                                                               AGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTG
                                                                                                                                                                                                                                   ATGAAGCCACACCAAGCCAGACCACGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG
                                                                                                                                                                                                                                                                                  TTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATG
 AAAGGGGCAAAAGTCCATTCTCATTTGGTC
                                    GGGGGTGGCAGAGGTCTCTTTGCTTCATTC
                                                                      ACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTT
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Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                   ABL62553;
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                                                                                                                                                RESULT 11
ABL62553/c
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                                                                                                                                                                                                                                                                                                                                                     the invention relates to isolated nucleic acids and proteins and cheir encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition of susceptibility comparable in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radiolamunosasays or enzyme linked immunososays (ELISA). Disorders which are diagnosed or treated immunososays (ELISA). Disorders which are diagnosed or treated include autoimmune disoases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. recordas system disorders e.g. arthored breast or liver, cardiovascular disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before cepenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present storage sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 CGCCTGTAÇATGGGCACAGCCACCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 TCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGAC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 TGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 GGATCAGTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 GCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 IGCCAACCAGTICATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                              invention relates to isolated nucleic acid molecules and their
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Pred. No. 3.7e-67;
0; Mismatches 135; Indels
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                                                                                                                                                        Ruben SM;
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71.0%;
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20000S-0254097
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 2000US-0251868
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Matches 331; Conservative
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08-DEC-2000; 2
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11-DEC-2000; 2
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517
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458 GCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAG
                         Human; cancer; colon; breast; ovary; oesophagus; kidney; thyrold;
                                                                                      518 GACTGGGCCAGCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTC 563
                                                                                                                             472 GATTGGTCTAGTAGTTAAAGGGGCAAAAGTCCATTCTCATTTGGTC 517
                                                                                                                                                                                                                                                                                                                                                                             Colon adenocarcinoma related gene sequence SEQ ID NO:890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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RESULT 12
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Best Local S
Matches 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 890; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells chemical agent to be tested for anti-neoplastic activity, ar determining a change in expression of a gene of a signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method (M1) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-188264/24
                                                                                                                          Human biallelic polymorphic DNA fragment WI-13859
                                                                                                                                                                                                                       AAX10492 standard; DNA; 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 247 BP; 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agent to be tested
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              Homo sapiens
                                                            autoimmune
                                                                            detection;
                                                                                           Polymorphism; biallelic; human;
                                                                                                                                                         30-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                            187
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Weaver Z;
                                             marker;
                                                          phenotypic typing; characteristic; infection;
disease; cancer; inflammation; drug; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                       (first entry)
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Pred. No.
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                                                                                         forensic;
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                                                                                         paternity testing;
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                                                          hereditary; medicament;
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Best Local :
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                                                                                                                                                                                                                                     haemorrhagic telangiectasia, familial colonic polyposis, Ehlers Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer; diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, yon Willebrand's disease, tuberous scierosis, hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid segments from the human genome -determining polymorphic forms for use in e.g. forensics, patesting or phenotypic typing for disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                    Sequence
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                                        133
   742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           markers which have been isolated using the in AAX09121-X10268. The base occupying the
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                                                                                                               Conservative
                                                                                                                                                                                    B₽;
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                                                                                                                                16.0%;
99.2%;
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                                                                                                                                Score 132.6; DB 19; Pred. No. 4.1e-31;
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                                                                                                               Mismatches
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            cytostatic; cardi
                  Human; immunosuppressive; antiarthritic; ds; antirheumatic;
                                             07-NOV-2001
                                                           AAS26708;
                                                                        AAS26708 standard; DNA;
                               Human
                                                                                                                     802
                               genomic
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                                                                                                        TTCTGACAAATAA 1
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                                                                                                                                  (first entry)
                               DNA
            lant; vasotropic;
                               encoding
                               partial novel
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     virucide; fungicide;
                               secreted
                               protein,
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neuroprotective;

e; fungicide; arthritis;

opthalmalogical;

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additive; preservative; antiproliferative. PR 25-589-2000 20008-01344 O GEO1441 PR 26-589-2000 20008-01344		200000	0000; 200 0000; 200 0000; 200 0000; 200 0000; 200	000; 200					lens. 322-A2. 301.	₩ #
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086968610097564467664151109875110987565448	01-DEC-2000; 2000US-02 01-DEC-2000; 2000US-02 05-DEC-2000; 2000US-02 05-DEC-2000; 2000US-02 05-DEC-2000; 2000US-02 06-DEC-2000; 2000US-02 06-DEC-2000; 2000US-02 08-DEC-2000; 2000US-02	17-NOV-2000; 20000S-02 17-NOV-2000; 20000S-02 17-NOV-2000; 20000S-02 17-NOV-2000; 20000S-02 17-NOV-2000; 20000S-02 17-NOV-2000; 20000S-02	R 17-NOV-2000; 2000US-0. R 17-NOV-2000; 2000US-0.	R 08-NOV-2000; 2000US-03 R 17-NOV-2000; 2000US-03	08-NOV-2000; 20000S-02 08-NOV-2000; 20000S-02 08-NOV-2000; 20000S-02 08-NOV-2000; 20000S-02 08-NOV-2000; 20000S-02 08-NOV-2000; 20000S-02	08-NOV-2000; 2000US-02	20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02 20-OCT-2000; 2000US-02	29-SEP-2000; 2000US-02 29-SEP-2000; 2000US-02 02-OCT-2000; 2000US-02 02-OCT-2000; 2000US-02 02-OCT-2000; 2000US-02 02-OCT-2000; 2000US-02 13-OCT-2000; 2000US-02	26-SEP-2000; 2000US-02 27-SEP-2000; 2000US-02 27-SEP-2000; 2000US-02 29-SEP-2000; 2000US-02 29-SEP-2000; 2000US-02 29-SEP-2000; 2000US-02	25-SEP-2000; 2000US-02 25-SEP-2000; 2000US-02

nootropic;

ocular disorder,

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RESULT 14
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence is a genomic DNA encoding a partial novel secretary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                      AAS26709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID No 1682; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding 461 h diagnosing, preventing, treating or ameliused as food additives or preservatives
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Human genomic DNA encoding partial novel secreted protein,
                                     07-NOV-2001
                                                                      AAS26709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                             AAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                  GATGAAGAGCAACTCAGTCCCAAACTACAGTTCTTGTTGACCAGTGGAACTGTG
                                                                                                      standard;
                                                                                                                                                                                                                          AGCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTC
                                                                                                                                                                                                                                                              ACTCCCAACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCT
                                                                                                                                                                                                                                                                                TCACCCAGCAACACACTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTG
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2000US-0251990.
2000US-0254097.
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                                    (first entry)
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Pred. No. 6.1e-24;
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 Seq ID 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
     vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzhelmer's disease; infection; ocular disorcorneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-200
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01-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food additive; preservative; antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US01341
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2000US-0232081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; antirheumatic;
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2000US-0251856

05-DEC-2000; 06-DEC-2000; 08-DEC-2000;

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hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotrals. The polypeptides can also be used as food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage and in chemotrals, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They rate are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunosasays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID No 1683; 980pp; English
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                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                   2000US-0251990
2000US-0254097
                                                                                                                                                                                  2001US-0259678
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                                                                                                                                                                                                                                                                                                                      WPI; 2001-488783/53
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08-DEC-2000;
08-DEC-2000;
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407 AAGTITGAGGGGAACAAACAACGGGACITCAACAAGAACITCAICCIGACGGCCCAGGCC 347 GTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTTGTCATCTGTGGATCAGTG 2140 AAGTITGATGGAAACAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCC TCACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCC AGTAGTTAAAGGGGCAAAAGTCCATTCTCATTTGGTC 1984 AGCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTC 563 467 527 pp à g g ò 용

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AAS75617 standard; cDNA; 1035

RESULT 15 AAS75617 ID AAS756 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynomic prices are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
P-PSDB; ABG11430.
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                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 11421; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1035 BP; 318 A; 219 C; 222 G; 276 T; 0 other;
                                                                                                                                                                                                           114 CATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCA 173
                                                                                                                                          174
                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                              134;
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AGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTT
                        ATGTCTACTACACCACCATGGATAAGGGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCA 233
                                                                                                                                                                                    ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA
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                                                                                                                                                                                                                                                                                · Conservative
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73.6%;
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0; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                     Indels
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Search completed: June 28, Job time: 215.801 secs 2003, 01:09:32

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                   Score
                                                                  847
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Match
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1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compagen Ltd.
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AL539324 AL539324
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AL596633 DKFZP313A
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ALIGNMENTS

	FEATURES Source	AUTHORS TITLE JOURNAL COMMENT	SOURCE ORGANISM ORGANISM	RESULT 1 AL539324 LOCUS DEFINITION ACCESSION VERSION
/organism="Homo Sapiens" /db_xref="taxon:9606" /clone="CSODF03xYD22" /clone=_ib="LTI_FL013_FBrn1" /clone_jbp="LYI_FL013_FBrn1" /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)" /lab_host="DH10B"	BP 191 9106 EVRY cedex - France Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr. Location/Qualifiers 1. 934	11, W.B., GRUDET, C., JESSEE, J. and Polayes, J. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Seguençage	human. human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 934)	AL539324 934 bp mRNA linear EST 16-FEB-2001 AL539324 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF034YD22 5 prime, mRNA sequence. AL539324 AL539324 I GI:12868435

BASE COUNT

Query Match Best Local Matches 892;

138

198

63

900 1037

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678 AAACTAAATTTCTTTAATATTTTCTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTT
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                                                                                                                                                                                                                        TGGAGCATTGCCCTCTAAGAGCTTTAAAACTATTTTTTACATGCCTTATATACATTCCA 797
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                                                               CTAATGACATTCTTATAATAATATTAAACACATGATCTTGGTACTAACATACTCACTGTG
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http://fulllength.invitrogen.com"
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AL548271 LTI_NFL006_PL2
prime, mRNA sequence.
AL548271
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Unpublished (2001)
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Mammalia; Eutheria;
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 TGGACAAGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGGTGGATGCCCTAAATA
                     TGGACAAGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                       enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen. 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end
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/note="Vector: pCMVSPO
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/clone_lib="LTI_NFL006_PL2".
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96.8%;
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www.genoscope.cns.fr

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Homo sapiens
Eukaryota; Metazoa; Chordata; Crania...,
Mammalia; Butheria; Primates; Catarrhini;
1 (bases 1 to 993)
NIH-MGC http://mgc.nci.nih.gov/.
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM12891 row: j column: 23
High quality sequence stop: 717.
Location/Qualifiers
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AGENCOURT_6763695 NIH_MGC_68
5', mRNA sequence.
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                    T-GGTTATTAGGTTAATTTTCTAGTAAAACACGTTGCCTGTTTTCAGTTAACACTGGTAA 1007
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                                                                                   TATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAAGTGGAGTTTTT
                                                                                                                                              ATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAAAAATAAAATCTTTT
                                                                                                                                                                                                                                                                       GTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGAGCTTTAAAACT
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                                                                   TATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAAATGGAGTTTTT
                                                                                                                                                                                            ATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATATATTAAACAC
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821 948 888

701 828 641 768 581 708 521

761

648

461 885 401

341 468 408

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348

161 288

221

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/clone_"IMAGE:5792758"
/clone_lib="NIH_MGC_68"
/clone_lib="NIH_MGC_68"
/clsue_type="large cell carcinoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
                                                                                              Technologies.
                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                    71.9%;
Score 824.4; DB
Pred. No. 1e-196;
0; Mismatches
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                                       DB 14; Length
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Indels

4

Gaps

101

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                                                                                                                                                  122 AACACACTGCTACAAGGTCCCAGATGGCCACGTCTCTGGATTTTAAAACTTATGTAGATC
                                                                                                                                                                                                                              72 GATCATTCCGCAGCCCTGCGGACCGGACACGTGAGGAGGTAGTGACGCCGACACTGCCAG 131
                                                                                                                                                                                                                                                                                                                                      790;
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DKFZp313A1822_r1 313 (synonym: hlcc2) Homo
DKFZp313A1822 5', mRNA sequence.
AL598693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone (DKFZp313A1822) is available at the RZPD in please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Bmail s. wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST (Duesterhoeft, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 793)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No si sequence available
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                                                                                                                                                                                                                                                                                                                                                   Similarity
                                             GACGGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGAAATGCTG
                                                                                                     AGGCATGTAGAGCTGCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGAA
                                                                                                                                                                  AACACACTGCTACAAGGTCCCAGATGGCCACGTCTCTGGATTTTAAAACTTATGTAGATC
                                                                                                                                                                                                                                                                                        GAGAATGGGAGGGTGGAAAATTTTGTGCGTTTGGCGGGTTTCGCTCTCCATAAGTATT 71
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                                                                                                                                                                                                              GATCATTCCGCAGCCCTGCGGACCGGACACGTGAGGAGGTAGTGACGCCGACACTGCCAG
TTTCAGGGCTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGG
                                                                                      AGGCATGTAGAGCTGCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGAA
                                                                                                                                                                                                                                                                          GAGAATGGGAGGGTGGAAAATTTTGTGCGTTTGGCGGGTTTCGCTCTCTTCATAAGTATT
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                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                      Conservative
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cDNA-collection"
1  160 c  172 g  241 t  1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="DKFZp313A1822"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                   68.9%;
99.7%;
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                                                                                                                                    Zhao, M., Song, H., Li, N., Direct Submission
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                                                                                                                                                                                           Zhao, M., Song, H., Li, N.,
A novel gene expressed i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens BM025 mRNA,
AF212223
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 /organism-"Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="bone marrow"
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612. CATTAGTTCCAGCAATTGAAATTTATGTGAAATTATTTTGATTGTAGAAGCACTATAATAT
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1 (bases 1 to 881)

Zhang, O.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G., Zhang, O.H., Ye, M., Wu, X.Y., Xu, X.R., Han, Z.G., Zhang, J.W., Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W., Tao, J., Huang, O.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoieti
Submitted (08-DEC-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong Shanghai 201203, People's Republic of China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGTTTGGAGCATTGCCCTCTAAGAGCTTTAAAACTATTTTTTTACATGCCTTATTTAC
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                                                  ATTCTTATAATAATAATAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGC
                                                                 ATTCTTATAATAATAATAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGC
                                                                                                       TGCCCTCTAAGAGCTTTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGAC
                                                                                                                TGCCCTCTAAGAGCTTTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGAC
                                                                                                                                                         TTTCTTTAATATTTTCTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCAT
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/db_xref="G1:9437513"
/db_xref="G1:9437513"
/translation="MDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ
/translation="MDKRRRALTRLYLDKATLIWNGNAVSGLDALNNFFDTLPSSEFQ
VNMLDCQPVHEQATQSQTTVLVVTSGTVKFDGNKQHFFNQNFLLTAQSTPNNTVMKIA
SDCFRFQDWSSS"
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/product="BM025"
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Mammalia; E
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AU123481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1532-3 Yana, Kisarazu,
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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HRI human cDNA project (Ota,T.,
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Helix Research Institute
Kisarazu, Chiba
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               GCCAGTTTGGAGCATTGCCCCTCTAAGAGCTTTAAAAACTATTTTTTTACATGCCTTATATA
                                                          TGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTGTCAGCACCTTTTCTAGCAGCT
                                                                         TGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTGTCAGCACCTTTTCTAGCAGCT
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 781)
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NT2RM2 Homo sapiens
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precursor cells"
129 c 138 g 278 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="NT2RM2000386"
/clone_lib="NT2RM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.6%;
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Nakamura,Y., Nishikawa,T., Nagai
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Nagai,T., Suzu
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Qy	Query Ma Best Loc Matches	BASE COUNT ORIGIN	: () ()	FEATURES	*		COMME	TITLE	REFERENCE	KEYWORDS SOURCE ORGANISM	ACCESSION	RESULT 7 AU137118 LOCUS	Qy 10	Qy . 10	Qy S	Оу 9 Db 4	Qy 8	Qy 7
30 AGAACACACTGCTACAAGGTCCC-AGATGGCCACGTCTCTGGATTTTAAAACTTATGTAG 188 	Query Match 61.6%; Score 706.2; DB 9; Length 770; Best Local Similarity 97.1%; Pred. No. 5.3e-167; Matches 748; Conservative 0; Mismatches 18; Indels 4; Gaps 3;	/Clone_11D="PLACE1" /tIssue_type="placenta" /note="Vector: pME18SFL3" 237 a 157 c 139 g 232 t 5 others	/organi/db_xrc	neila meseatum institute: Location/Qualifiers 1 770	Email: genomics@hri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and	Tel: 81 438 - 22 - 3975 Fax: 81 438 - 52 - 3986	Genomics Laboratory Genomics Laboratory Helix Research Institute 1532-3 Yana. Kisarazu Chiba 292-0812 Japan	(200) Coordi	Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 770) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and		CT 10007657	AU137118 770 bp mRNA linear EST 02-AUG-2002	1091 GAATTGCATATAGAGATGTTCAGTGGTCGTTTTTCATTTTAAGTAATTTTTGTTTT 1146 	1031 TCAAATCAGTTCAGTGAAAATAGTACAGATTTAGGTTTACATAACTACTCTGACATACTG 1090	971 GTAAAACACGTTGCCTGTTTTCAGTTAACACTGGTAATGCCATTTTAATATATGGCCTTTT. 1030 	911 CAGCACAATATAACACTCTGGGAAGAAGTGGAGTTTTTTGGTTATTAGGTTAATTTTCTA 970 	851 CACTGTGAACCCAGCCTATTGCAAAAATAAAATCTTTTTATAATATTATCTATGGGATGT 910	791 CATTCCACTAATGACATTCTTATAATATATATAAACACATGATCTTGGTACTAACATACT 850
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                                                        TACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAATG
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/tlssue_type="lelomyosarcoma"
/tlsb_host="DH108 (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6;
Site_2: Sall; Cloned unidirectionally. Pri
Average insert size 2.1 kb. "
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/db_xref="taxon:9606"
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Pred. No. 4.1e-161;
""" amatches 7;
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Best Local Similarity
Matches 722; Conserv
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Clone distribution: MGC clone distribution informat found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                     ATTGCCTTATAGTGAGTTCCAGGTCAATATGTTAGATTGCGAACCAGTTCATGAGCAAGC
                                                                                         ATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATGAGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-Xhol (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT.5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMI/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

a 144. c 156 g 244 t
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/clone_lib="NIH_MGC_96"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="hypothalamus"
/lab_host="DH10B"
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98.0%;
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                                                                                                                                                                                             Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 721)
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AV714243 DCB Homo
AV714243
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Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M
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                 199
                                                                                                                                                                                   clone
                                                                                                                                                                hanzg@chgc.sh.cn
lone is available at CHGC
Location/Qualifiers
                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCBASG08"
                                             /clone_lib="DCB"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
            /note="Vector: pTriplEx2; Site_1: sfilA; 146 c 170 g 206 t
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies,
                                                   Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Nammalia; Eutheria; Primates; Catarrhini Lobases 1 to 743)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1460 row: m column: 08
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 ATTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATAATAATAACAC
                                     GTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGAGCTTTAAAACT
                                                                      GTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCCTCTAAGAGCTTTAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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lone_11b="NIH_MGC_116"
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Query Match
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National Institutes of Health, M
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1 (bases 1 to 819)
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Plate: LLAM11745 row: n column: 06
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Clone distribution: MGC clone distribution information can
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ATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATGAGCAAGC
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/t1ssue_type="hypothalamus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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602325770F1 NIH_MGC_90
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 878)
                                                                                                                                                                                                                                                                mRNA sequence.
BG035698
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                                                              found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLAM10140 row: 1 column: 18
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National Institutes of Health, Mammalian
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                                                                                                                                                               Jnpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
               /organism="Homo sapiens"
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                                                  TGGACCATACTGGAATTGCCTATAGAGAATGTTCAAGGGGTCGTTTTCATTTTAAGTAAT
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/lab_host="DH10B (phage-resistant)"
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95.58;
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Pred. No. 2.4e-143;
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                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J
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Ludwig Institute for Cancer Research
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CAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAACAACAACAT
                                                                                           AATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTCT
                                                         ACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCAATATTTACTATGAGACA
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ect. This entry can be seen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inote-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A.mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone_lib="HT0342"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.6e-143;
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SOURCE
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                             (http://www.ludwig-org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-HT0342-
190201-007-h05&t3=2001-02-19&t4=1)
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          /dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
//note="Organ: head_neck; Vector: puc18; Site_1: SmaI; A mini-library was made by cloning products
// Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
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/db_xref="taxon:9606"
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Db 6	Оу 7	Db	Qy .	Db . 4	Qy 5	Db 4	Оу :	. ad	0у 4	Db 3	0у 4	Db 2	. Ωγ 3	Db 1	Qy 2	Db 1	0у 2	В	Оу 1	D	Qy 1	Best Loca Matches		BASE COUNT ORIGIN
02 TTTCTAGCAGCTGCAAGTTA	719 TTTCTAGCAGCTGCCAGTTTGGAGCAT 745	542 AGCACTATAATATGTGCTGAAACTAAATTTCTTTAATATTAACTATTCCTGTCAGCACCT 601	+3	482 TGCTCATTTTGGTCCATCAGTTCCAGCAATTGAAATTCATGTGAATTATTTTGATTGTAGA 541	599 TTCTCATTTGGTCCATTAGTTCCAGCAATTGAAATTTATGTGAATTATTTTGTATTGTAGA 658	422 ATTGCAAGTGATCGCTTTCCATTTTCAAGATTAGTCTAGTTAAAAGGGGCAAAAGTCCA 481	63	362 TTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCAACAATACTGTGTGGGAAG 421	479 TTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCAACAATACTGTGTGGAAG 538	302 CAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTGGATGGA	419 CAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGGATGGA	242 AGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCCAGTTCATGAGCAAGCA	359 AGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATGAGCAAGCA	182 AATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTCT 241	299 AATGGAAATGCTGTTTCAGGGGTGGATGCCCTAAATAATTTTTTTT	122 ATGGATAAAAGAAGACGGGACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGG 181	239 ATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGG 298	62 ACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCAATATTTACTATGAGACA 121	179 ACTTATGTAGATCAGGCATGTAGAGCTTGCTGAGGAGTTTGTCAATATTTACTATGAGACA 238	2 CCGACACTGCCAGAACACACTGCTACAAGGTCCCAGATGGCCACGTCTCTGGATTTTAAA 61	119 CCGACACTGCCAGAACACACTGCTACAAGGTCCCAGATGGCCACGTCTCTGGATTTTTAAA 178	_	53.3%; Score 611; DB	187 a 129 c 131 g '182 t

Search completed: June 28, 2003, 03:34:25 Job time: 1928.73 secs

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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ALIGNMENTS

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Query Match
Best Local Similarity
                                                                                                                                                                                                                  TELEFAX: 212-869-8864/
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 STRANDEDNESS:
TOPOLOGY: unk
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                   TELEPHONE: 212-790-9090
                                                                                                                                                                                 TYPE: nucleic acid
                                                                               NAME/KEY: misc_feature LOCATION: 2149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
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                                                                                                                                                                                                 2692 base pairs
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1155 Avenue of the Americas
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                                                                                                                                 unknown
PE: cDNA
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                                                               /note= "N=x=unknown nucleotide"
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 Score 40; DB 1;
Pred. No. 0.09;
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US-08-449-609-14
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APPLICATION NUMBER: US 0
FILING DATE: 23-MAR-1993
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                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      LOCATION: 2149
OTHER INFORMATION: /note-
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 76:LECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                    987 GTTTTCAGTTAACACTGGTAATGCCATTTTAATATATGGCTTTTTCAAATCAGTTCAGTG 1046
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Avenue of the Americas
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Karin B.
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                                                                                       Score 40; DB 2; Pred. No. 0.09;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
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PRIOR APPLICATION NUMBER: US 07/827,685
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
WO 92/14818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-FEB-1991
TORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 12-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO 9 FILING DATE: 12-FEB-1992
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                                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                        904-372-5800
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                                                                                       complement (234..782)
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3.4%; Score 39.4;
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 DB 1;
Length 1511;
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Best Local Similarity
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ZIP: 32606
ZIP: 32606
COMPUTE RADABLE FORM:
COMPUTER TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TYPER: IBM PC COMPATIBLE
TYPEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                                                                                                                                     TELEFAX: (904) 372-58
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                  MOLECULE TYPE:
)RIGINAL SOURCE:
NAME/KEY:
                                LOCATION:
                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                 ORGANISM:
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                                                                                                                                               TRANDEDNESS:
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2421 N.W. 41st Street, Suite A-1
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CDS
                               complement (18..218)
                                                                                 Amsacta moorei entemopoxvirus
                                                                                                                                unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.25
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Mismatches 106;
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Best Local Similarity
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                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Re
                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 07-DEC-1992
                                                                               APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991
                                                                                                                                  FILING DATE:
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 19-AU
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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852..1511
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                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerard H. Bencen
                                                                                                                              30-JAN-1992
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19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                Gerard H
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1. Michael E.

N: No. 5935777el Entomopoxvirus Expression System
INFORMATION
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                                                                                                                                               US 07/827,685
                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0,
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               UF114.C4
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Version

#1.

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1013 TAAAATATTATTATCATAATATATATATGCAATTCTTCTAAATTAACTAATTTTTTAA
833 TTTTCATTGATTAATTTTTTTTTGAAAAA 805
                                    948 TTGGTTATTAGGTTAATTTTCTAGTAAAA 976
                                                                                  893 TAAAATATTTATTAAAAATTATATCAGAATTTAGTAAATCCATTTTGATAATTTTATTTTT
                                                                                                                           888 TTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAAGTGGAGTTTT 947
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Pred. No. 0.1;
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ELEPHONE:

904-375-8100

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US-08-544-332-8
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Best Local Similarity
Matches 103; Conserv
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TYPE: DNA ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Moyer, Richard W. PPLICANT: Hall, Richard L.
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                                         ENGTH: 1511
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                                                                                                                                                                                                                                                                                                                                    E REFERENCE: UF114.C4.D1
                                                                                                                                                                                                                                                                                                                                                     LICANT: Gruidl, Michael E.
LE OF INVENTION: No. 6410221el Entomopoxvirus
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                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/107,755
FILING DATE: 1993-08-19
                                                                                                             FILING DATE: 1991
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/991,867 FILING DATE: 1992-12-07
                                                                                                                              FILING DATE: 1992-01-30 APPLICATION NUMBER: US 07/657,584
                                                                                                                                                             APPLICATION NUMBER: US 07/827,685
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                                                                                                                                                                                       PLICATION NUMBER: LING DATE: 1992-0
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-453-702B-206
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157 NUMBER OF SEQUENCES: 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blattner, Frederick R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 893 TAAAATATTTATTAAAATTATATCAGAATTTAGTAAATCCATTTTGATAATTTTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 828 CATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAAAAATAAAATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 768 TATTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATAATATTAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAAGTGGAGTTTT 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTCATTGATTAATTTTTTTTTGAAAAA 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGGITATIAGGITAATITICTAGIAAAA 976
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                  STRANDEDNESS: double
                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                 NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDDRESSEE: Quarles & Brady
                                                                                                                                                                                           ENGTH: 43360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09453702B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.3%;
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                                                                                                                                                                                                                                                                      (808)
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                                                                                                                                                                                                                                                    251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                   <Unknown>
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Pred. No. 0.1;
0; Mismatches 106;
Score 37; DB 4; Length 43360; Pred. No. 2.5; 0; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                               960296.95017
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Query Match
Best Local Similarity
Matches 115; Conserv

46.98;

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                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-453-702B-261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 261, Applicat Patent No. 6365723 GENERAL INFORMATION:
                                          Query Match
        Matches
                                                                                                                                                                                        TELEFAX: (608) 251-91
INFORMATION FOR SEQ ID NO: 261:
SEQUENCE CHARACTERISTICS:
                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22854 GTTATTCTTTGTACTTTGTACACATAATCATCTTTTGGGCCCATCTTTAATAAAGTGAACA 22913
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3:50 inch. 1.44Mb storage
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blattner, Frederick R
        al Similarity
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                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                         NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGTTCAGTGAAAATAGTACAGATTTAGGTTTACATAACTACTCTGACATACTGGAATT 1095
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                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Madison
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        Conservative
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Plunkett, u.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burland,
                      3.2%;
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                                                                                                                                                                                                                           251-9166
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     Score 37; DB 4; Length 45325; Pred. No. 2.5; 0; Mismatches 130; Indels
                                                                                         261:
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     Gaps
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Query Match
Best Local Similarity
Matches 146; Conser
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US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                TOPOLOGY: 1:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 10-SEP-1993
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23756 GTTATTCTTTGTACTTTGTACACATAATCATCTTTTGGGCCATCTTTAATAAAGTGAACA 23815
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1: 620 Newport Center Drive 18th Floor
Newport Beach
: California
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5993827
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                                                                                                                                                                                                                        19124 base pairs
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Miller, Louis H
                                                                                                                                                               linear
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Wellems, Thoma
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                       3.28;
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/487,826B
Score 36.8; DB Pred. No. 1.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    NIH121.001CP1
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                                          DB 2; Length 19124;
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US-09-641-638-651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/641,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING ITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM ILE REFERENCE: GENSET.051CP1
                                                            THER INFORMATION: exon
                                                                                                                           THER INFORMATION: exon
                                                                                     CATION: 5758..5880
                                                                                                                                                                                                                                                                                                                            HER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                              E/KEY: misc_feature
ATION: 1123..3123
                                                                                                                                                                                                                                                           ER INFORMATION: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6250 TATATAAATGAAAATATTTGTTATAATATAAATACATATATGCTACTATATAAATATTAA 6191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6310 CATTATAAATATATATATTCAAATATGAGTTATTAATAAAAATGTTCATGTTCTATATATT 6251
                                                                                                                                                    TION: 5552..5633
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OTHER INFORMATION: exon LOCATION: 6349..6509 OTHER INFORMATION: exon THER INFORMATION: exon NAME/KEY: allele LOCATION: 1559 OTHER INFORMATION: 10-508-245 THER INFORMATION: exon THER INFORMATION: exon OTHER INFORMATION: NAME/KEY: allele LOCATION: 2623 DTHER INFORMATION: OCATION: 2341 OTHER INFORMATION: NAME/KEY: allele LOCATION: 2323 OTHER INFORMATION: 10-511-337 THER INFORMATION: THER INFORMATION: 10-508-191 AME/KEY: misc_feature OCATION: 17555..20674 THER INFORMATION: exon OCATION: 16775..16945
THER INFORMATION: exon THER INFORMATION: exon THER INFORMATION: exon 11 THER INFORMATION: THER INFORMATION: 3'regulatory region THER INFORMATION: AME/KEY: allele OCATION: 1827 THER INFORMATION: 10-510-173 HER INFORMATION: 10-509-295 17063..17554 12854. [13023 12254..12340 13308..13429 6567..16667 6775..16945 12-206-81 10-512-36 10-511-62 10-513-352 10-512-318 10-509-284. 10-513-262 10-513-365 10-513-250 12 : polymorphic base C or : polymorphic base A or G polymorphic base A or G polymorphic base G polymorphic base C insertion of T variable motif ATTTA or TTTTTT deletion of C polymorphic base polymorphic base C or polymorphic base À or G polymorphic base C polymorphic base A or polymorphic base A or G G ę ٠<u>٥</u> or J

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Best Local Similarity 44.:
Matches 143; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Spiker, Steven TITLE OF INVENTION: MATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION
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Michalowski and Spiker
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                                                     Best Local Similarity Matches 142; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
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                                                                                                                                                 ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 AACCCAGCCTATTGCAAAAATAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACA 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      978 ACGTTGCCTGTTTTCAGTTAA 998
616 AGTICCAGCAATIGAAATTATGTGAATIATTITGATTGTAGAAGCACTATAAIATATGTGC 675
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Research Triangle Park
:: No. 6239264th Carolina
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Knechtle, Philipp
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TENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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Steiner, Sabine
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                                                                      Score 36; DB 4;
Pred. No. 0.68;
                                                         Mismatches 155;
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US-08-323-170B-1/c
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                                 Query Match
Best Local Similarity Matches, 147; Conserv
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                   FEATURE:
                                                                                                                                                     MOLECULE TYPE:
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                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/010,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                             9636 base pairs
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Two Embarcadero Center, 8th Floor
3.1%;
ilarity 47.0%;
Conservative
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IBM PC compatible
                                                                                                                                                                           linear
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Score 35.8; DB 1;
Pred. No. 2.7;
0; Mismatches 162;
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   162;
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                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                            NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015280-113110US
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/323,170 FILING DATE: 13-OCT-1994 NIOR APPLICATION DATA:
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                   NAME/KEY:
                                                                          ropology:
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CDS
149..9556
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US-08-991-677-11
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US-08-991-677-11
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Best Local Similarity
Matches 147; Conser
                                                                                                                                                                                                                                                                                                                                                           Query Match 3.1%;
Best Local Similarity 45.9%;
Matches 122; Conservative
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SEQ ID NO 11
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Patent No. 62521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1996-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/991,677A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: US 60/033,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chiang, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENGTH:
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                                                                          938 GTGGAGTTTTTTGGTTATTAGGTTAATTTTCTAGTAAAACACGTTGCCTGTTTTCAGTTA 997
                                                                                                                                                       878 TAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAA 937
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998 ACACTGGTAATGCCATTTTAATATAT 1023
                                                                                                                  840 AAAATTAATTTTAAATTAATAAACTTTTGAAGTCAAATATTCCAAATATTTCCAAAATA 899
                                                                                                                                                                                                 780 CTATTATTTTAAAAAATTTGTTGGTAAATTTTATCTTATATTTAAGTTAAAATTTAGAA 839
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                                       TTAAATCTATTTTGCATTCAAAATACAATTTAAATAATAAACTTCATGGAATAGATTAA 959
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960 CCAATTTGTATAAAAACCAAAAATCT 985 .

Search completed: June 28, 2003, 03:36:24 Job time: 64.6356 secs

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Post-processing: Minimum Match 0%
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Perfect score:
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Maximum DB seq length: 200000000
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score greater than or equal to the score and is derived by analysis of the total Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being priscore distribution printed

SUMMARIES

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ALIGNMENTS

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RESULT 1
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autoimmune haemolytic anaemia;
                     immune disorder; céll proliferative
urticaria; allergy; abnormal vesicle
                                                                                                              antiallergic; antidiabetic;
                                                                                                                                    antiarthritic; antiasthmatic;
                                                                                                                                                                                                     Human protein transport molecule (PTAM) encoding cDNA SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                        AAA08041;
                                                                 antiinflammatory;
                                                                                      dermatological; antianaemic;
                                                                                                                                                                                                                                                          19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                 AAA08041 standard; cDNA; 1146 BP.
                                                                                                                                                                                                                                                     (first entry)
                                                                 antiHIV;
                                                                                                                                    immunosuppressant;
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Human; protein transport molecule; PTAM; diagnosis; cytostatic; antirheumatic; osteopathic;
c; hepatotropic; antigout; secretory disorder; antiarteriosclerotic;

Homo sapiens.

09-MAR-2000.

WO200012703-A2

26-AUG-1999; 99WO-US19616.

27-AUG-1998; 98US-0098206

(INCY-) INCYTE PHARM INC.

Tang YT, Lal P, Bandman O, Yue H, Corley NC, Guegler KJ

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecules (PTAMS) given in AAY82317 to AAY82324. The PTAMS have cytostatic, antiarthritic, antiasthmatic. immunocurrent and antiarthrical control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antirheumatic, osteopathic, dermatological, antianaemic, antipsoriatic, hepatotropic, antigut, antiinflammatory and antiHIV activities, and regulate protein transport. PTAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 74; 75pp; English.
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expression or activity of PTAM. PTAM polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic, antiallergic, antidiabetic, antilipaemic,
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                                                                                                                                                            occurring genomic
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Pred. No. 4.2e-291;
; Mismatches 0;
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  15-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; cDNA; 2581
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                                                                                                                                                                                                                                                                                                                                                                                                                               associated protein 16 coding sequence.
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  2000CN-0114918
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                                                                                                                                                                                                                Location/Qualifiers 147..575
                                                                                                                                                                                                                                                                                                                                                                          protein 16;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding NTF2 associated protein 16. The sequences can be used cancer and HIV infection; as well as other diseases. The the coding sequence of the invention.
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      TATGTGCTGAAACTAAATTTCTTTAATATTTCTATTCCTGTCAGCACCTTTTCTAGCAG
                                                 ATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTAGTGAAGGGGCAAAAGTCCATTCTCATTTG
                                                                                                         AGAACTTCCTGCTGACTGCTCAGTCCCACTCCCAACAATACTGTGTGGAAGATTGCAAGTG
                                                                                                                                            CTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTGACACATTGCCTTCTAGTGAGTTCC
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                                                                       ATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAGGGGCCAAAAGTCCATTCTCATTTG
                                                                                                                                                                                                                                                                                                                                                                                            GGAGAGAATGGGAGGGTGGAAAATTTTGTGCGTTTGGCGGGTTTCGCTCTTCATAAGT
                                       GTCCATTAGTTCCAGCAATTGAAATTTATGTGAATTATTTTGATTGTAGAAGCACTATAA
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The present sequence
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The invention resource a nucleotide sequence
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25-MAY-2000;
09-JUN-2000;
                                     Claim 1;
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                                                                                                                                                                                                                                                             Homo sapiens
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Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer stage of prostate cancer
                                                                   WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                       Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                           prostate expression marker
                                                                                                                  MILLENNIUM PREDICTIVE
Page 4644; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCAAATCAGTTCAGTGAAAATAGTACAGATTTAGGTTTACATAACTACTCTGACATAC
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(d) assessing the efficacy of a therapy for inhibiting prostate a patient;
(e) selecting a composition for inhibiting prostate cancer in (f) assessing the prostate cell carcingenic potential of a (g) determining whether prostate cancer has metastasized in (h) assessing the aggressiveness or indolence of prostate ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monitoring whether a patient is afflicted with prostate cancer; monitoring the progression of prostate cancer in a patient; assessing the efficacy of a test compound to inhibit prostate cer in a patient; assessing the compound to inhibit prostate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1093;
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                                                                                                                                  GCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGAGCTTTAAAACTATTT
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                                                TTTTACATGCCTTATATACATTCCACTAATGACATTCTTATÄATAATATTAAACACATGA
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TCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAAAAATAAAATCTTTTTATA
                                                                                                                                                                                                     TGTAGAAGCACTATAATATGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTGTCA
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07-FEB-2001 primer; detection; diagnosis; antisense

29-JUL-1999; 99JP-0248036. 27-AUG-1999; 99JP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-0241899 (HELI-) HELIX RES INST 28-JUL-2000; 2000EP-0116126

Ota T, Ishii S, Isogai T, 3, Sugiyama Nishikawa T, Wakam hikawa T, Wakamatsu Hayashi K, A, Nagai K, Salto aito K, Otsuki Yamamoto T;

Primer sets for synthesizing polynucleotides, particularly the full-length cDNAs defined in the specification, and for the deand/or diagnosis of the abnormality of the proteins encoded by full-length the 5602 he detection d by the

8 Ħ 2537pp B ROM; English

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1064; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs the primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3693 represent oligonucleotides, all of which are used in the exemplification of the present invention.
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                                                                             GACATTCTTATAATAATATTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCC
                                                                                                                                                           AAATTTCTTTAATATTTCTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAG
                                                                                                                                                                                                                                                                                                                       GCAATTGAAATTTATGTGAAATTATTTTGATTGTAGAAGCACTATAATATGTGCCTGAAACT
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                                                                                                                                                                                                                   AAATTTCTTTAATATTTTCTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAG
                                                                                                                                                                                                                                                                                                 GCAATTGAAATTTATGTGAATTATTTTGATTGTAGAAGCACTATAATATGTGCTGAAACT
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Pred. No. 2e-269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2001
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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, cc rabbits, goats, horses, cats, dogs, chickens or sheep. They cc rabbits, goats, horses, cats, dogs, chickens or sheep. They cc rabbits, goats, horses, cats, dogs, chickens or sheep. They cc are also used in diagnosing a pathological condition or susceptibility compared to a pathological condition. Antibodies to the proteins can also cc used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked communosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. neoplasms of the breast or liver, cc gradiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, or increase and funging call culture of primary tissues, to crepense isted in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to crepensate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins,
                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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01-SEP
01-SEP
01-SEP
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                                                                                                                            14 - AUG -
18 - AUG -
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encoded secreted proteins. The nucleic acid molecules and their corrected proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They can also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also compared to a pathological condition. Antibodies to the proteins can also compared to include autoimmunoassays e.g. radioimmunoassays or enzyme linked conclude autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. 
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Best Local Similarity
Matches 749; Conserv
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                                                                                      GATGAAGAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTG
  AAGTTTGATGGAAACAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCC
                                                                                                                                  GTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTG
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2000US-0251856.
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                                                                                                                                                                           Score 747.2; DB 22
Pred. No. 5.7e-186;
0; Mismatches 3;
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20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000;

2000US-0246474

08-NOV 08-NOV 17-NOV 17-NOV

-NOV-2000;

17-NOV-2000;

515 ACTCCCAACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCT

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-NOV-2000;

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RESULT 7
AAS26709/c
ID AAS26709 standard; DNA;
                                                                                                                                                                         Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
                                                02-AUG-2001.
                                                                                                                          cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative
31-JAN-2000; 2000US-0179065.
                        17-JAN-2001; 2001WO-US01341
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        New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
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include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, hyperproliferative disorders e.g. cardiovascular disorders e.g. anglogenesis, nervous system disorders e.g. alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunocern. The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used prevent, treat or ameliorate a medical condition in e.g. humans, mirabbits, goats, horses, cats, dogs, chickens or sheep. They diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or nt, lipid, protein, carbohydraté, vitamins, other nutritional components. The present NA encoding a partial novel secreted protei or treated protein mice 6 of f

AAGTTTGATGGAAACAACAACATTTCTTCAACCAGAACTTCCTTGCTGACTGCTCAGTCC TATTITCTATICCTGICAGCACCITIICTAGCAGCIGCCAGTITGGAGCATIGCCCTCTA AGTAGTTAAAGGGCCAAAAGTCCATTCTCATTTGGTCCATTAGTTCCAGCAÀTTGAAATT ACTCCCAACAATACTGTGGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCT GAAGTGGAGTTTTTTGGTTATTAGGTTAATTTTCTAGTAAAACACGCTTGCCTGTTTTCAG AAATAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAA ATAATATTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAA ATAATATTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAA **AAGTTTGATGGAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCC AAATAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAA** Score 747.2; DB 22; Pred. No. 5.7e-186; 0; Mismatches 3; 22; Indels Length 8919; 0, 1781 514 2141 454 1601 1661 934 172] 874 1961 2021 2081 694 634 0

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RESULT 8
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13632 to AAH13632 and AAH13632 and AAH13632 and AAH13632 to AAH13632 and AAH13633 to AAH13632 and AAH13632 to AAH13632 and AAH13633 to AAH13632 and AAH13633 to AAH13632 and AAH13632 to AAH13632 and AAH13633 and AAH13633
                                                                                                                                                                                                                                                                                                                                                                                                                                  of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 3849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakama
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Wakamatsu
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A, Nagai K,
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(, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; gene therapy;
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23-AUG-2000;
                                                                                                                                                                                                                                                DNA encoding
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                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                      Human; chromosome
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                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                          11-OCT-2001
                                                                                                                                                                                                         food supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 GATTGCCAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACC
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                                                      2000US-0540217
2000US-0649167
Liu C,
                                                                                                                                                                                                                                                novel human diagnostic protein #11421
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                                                                                                                                                                                                                                                                                                                                cDNA; 1035
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97.58;
Tang YT;
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                                                                                                                                                                                                          imaging;
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                                                                                                                                                                                                         apping; gene therapy; forensic
diagnostic; genetic disorder;
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1.2e-119;
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cc for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical cdisorders involving aberrant protein expression or biological activity. (CC The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess blodiversity cand to produce other types of data and products dependent on DNA and candino acid sequences. AAS64197-AAS94564 represent novel human cc diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cc at ftp.wipo.int/pub/published_pct_sequences.
XBXBXAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclaotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques.
                Human protein
                                                    19-JUN-2000
                                                                                                                            AAA08036 standard; cDNA; 830
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P-PSDB; ABG11430.
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                                                                                                                                                                                                                              CAGGGCTGGATGCCCTAAATAATTTTTTTTTGACACATTGCCTTCTTAGTGAGTTCCAGG
                                                                                                                                                                                                                                                                    CAGGGCTGGATGCCCTAAATAA - - TTTTTTTGACACATTGCCTTC - TAGTGAGTTCCAGG
                                                                                                                                                                                                                                                                                                          GGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGAAATGCTGTTT
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                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to isolated polynucleotide (I) and I) sequences. (I) is useful as hybridisation probes.
              transport molecule (PTAM) encoding cDNA SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 A; 219 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.98;
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0; Mismatches
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В õ 밁

Matches

326;

Conservative

0;

Mismatches

124;

Indels

0

Gaps

114

CATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCA CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTTGTCA

173 221

ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA

ATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCA

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234

293 341 233 281

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Query Match
                                                                                                                                                                                                                                                         hepatotropic, antigout, antiliflammatory and antiHIV activities, and regulate protein transport. PTAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased expression or activity of PTAM. PTAM polynucleotides are useful for diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle trafficking, such as allergies, asthma, untidaria and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; protein transport molecule; PTAM; diagnosis; cytostatic; antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic; antiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic;
                                                                                                                               haemolytic anaemia. Anti-TTAM antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecules (PTAMS) given in,AAY82317 to AAY82324. The PTAMS cytostatic, antiarthritic, antiasthmatic, immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; antiHIV; protein transport regulator;
immune disorder; cell proliferative disorder; secretory
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 70; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antirheumatic, osteopathic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic, antiallergic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA08035 to AAA08042 encode the human protein transport-associated
  Local
  Similarity
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                                                                 830 BP;
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                                                                 198 A; 208
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                                                                                                             genomic
22.0%;
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Patterson C;
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                                                                 Ç
                                                                                                             sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological,
Pred. No.
                    Score 251.6; DB 21; Length
                                                                 195 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trafficking; asthma;
                                                                 229 T; 0 other;
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  4e-56
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02-MAR-2000;
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04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyrostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2001
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                                                                                                                                                                            28-JUN-2000;
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                                                                                                                                                                                                        19-MAY-2000;
                                                                                                                                                    -JUL-2000
                                                                                                                                                                                                                                 -MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 GGGGGTGGCAGAGGTCTCTTTGCTTCATTC
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2000US-0180628.
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2000US-0246477.
2000US-0246478.
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are also used in diagnosing a pathological condition or susceptibility
to a pathological condition. Antibodies to the proteins can also
be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
immunosorbant assays (ELISA). Disorders which are diagnosed or treated
include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sumburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-2000
08-NOV-2000
08-NOV-2000
                                                                                                                                                                                                                                                    encoded secreted proteins. The nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g., humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnocian and their contractions.
                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000
17-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 461 human sec
diagnosing, preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ( HUMA - )
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d additives o
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                                                                         17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
                                    09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                         ABV07047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as a food additive or pres
capabilities, fat content,
minerals, cofactors and ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regenerate tissues as a food additive
                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                     13-SEP-2002
                                                                                                                                                                                                                                                                                                                                               ABV07047
                                                                                                                                  20-FEB-2001;
                                                                                                                                                             23-AUG-2001
                                                                                                                                                                                         WO200160860-A2
                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 7038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGAAACAAACAATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCAGTCCCCA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGTGGCAGAGGTCTCTTTGCTTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGGGCAAAAGTCCATTCTCATTTGGTC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAGCCACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGGAACAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCA
                                  2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                      2000US-183319P
                                                                                                                                  2001WO-US05171
                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or preservative to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and in chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nt, lipid, protein, carbohydrate other nutritional components. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 251.6; Db ...,
Pred. No. 4.1e-56;
Pred. No. 4.1e-56;
                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polypeptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                               528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         864;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

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                                                                                                                                                                                                                                    ABV36989,
                                                                                                                                                                                                                                             RESULT 13
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Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) companies to a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer in a patient,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlegel R,
                                                                                                                                                         Human
                                                                                                                                                                               16-SEP-2002
                                                                                                                                                                                                    ABV36989
                                                                                                                                                                                                                         ABV36989 standard; cDNA; 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for detecting
                                                                                  WO200160860-A2
                                                                                                                           Human; prostate pharmacogenomic
                                        20-FEB-2001; 2001WO-US05171.
                                                             23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    selecting a composition for inhibiting prostate cancer in a patten assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patient;
                                                                                                                                                                                                                                                                                                                        124
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                                                                                                                                                                                                                                                                                                                                                                                                           244
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.2%;
il Similarity 100.0%;
220; Conservative (
                                                                                                                                                          prostate
                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                 plated nucleic acid molecule associated with cancerous state cells and correlating with presence of prostate cancer, use
                                                                                                                                                                                                                                                                                                                                                                                                           AATATATGGCTTTTTCAAATCAGTTCAGTGAAAATAGTAC
                                                                                                                                                                                                                                                                                                                                     AGGTTAATTTTCTAGTAAAACACGTTGCCTGTTTTCAGTTAACACTGGTAATGCCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                              GGTACTAACATACTCACTGTGAACCCCAGCCTATTGCAAAAATAAAATCTTTTTATAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 1144-1145;
                                                                                                                                                                                                                                                                                                                         AGGTTAATTTTCTAGTAAAACACGTTGCCTGTTTTCAGTTAACACTGGTAATGCCATTTT
                                                                                                                                                                                                                                                                              AATATATGGCTTTTTCAAATCAGTTCAGTGAAAATAGTAC
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        2000US-183319P.
2000US-189862P.
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                                                                                                                                                                             (first entry)
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                                                                                                                                                         expression
                                                                                                                           marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 C;
                                                                                                                          cytostatic; carcinogen;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monahan
                                                                                                                                                         marker cDNA 36980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 220; DB; Pred. No. 5.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 G;
                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid molecule (I) comprising s 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e-48;
s 0;
                                                                                                                                     pharmacodyanamic
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                                                                                                                                                                                                                                                                                                   1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245;
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                                                                                                                                      marker;
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                                                                                                                                                                                                                                                                                                                                                                                                           185
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13-FEB-2002 CDNA #1201 e Human; colon

tumour

protein;

colon cancer;

gene

therapy; cytostatic;

SS

encoding

of.

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human

colon

(first

entry)
portion

Homo sapiens

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RESULT 14
AAS58525
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a nucleotide sequence given in Tables 1-9 (ABV0001 specification or its complement (I) is useful for (a) assessing whether a patient is afflicted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 7616; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with prostate cells and correlating with presence of prost for detecting presence of prostate cancer, stage of I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE
AAS58525
                                 AAS58525 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   selecting a composition for inhibiting prostate cance assessing the prostate cell carcinogenic potential of determining whether prostate cancer has metastasized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monitoring the progression of prostate cancer in a pati
assessing the efficacy of a test compound to inhibit procer in a patient:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining whether prostate cancer assessing the aggressiveness or inde
                                                                                                                                                             1017
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                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                897 TATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAAGTGGAGTTTTTTGGTTATT
                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                           220;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                             AATATATGGCTTTTTCAAATCAGTTCAGTGAAAATAGTAC
                                                                                                                                                                                                                                       AGGTTAATTTTCTAGTAAAACACGTTGCCTGTTTTCAGTTAACACTGGTAATGCCATTTT
                                                                                                                                                                                                                                                                            Conservative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                 cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š,
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                                   318
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 220;
Pred. No.
                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (I) is useful for:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      indolence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potential of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 441;
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useful
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Search completed: June 28, 2003, 01:09:33
Job time : 296.199 secs
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Db
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                                                                                                                                                                                                                                                                                                                                                         proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynuclectides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynuclectides sequences are also useful ir gene therapy. AAS57325-AAS58880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
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                                                                                                                                                                                                                             New colon tumour proteins and related nucleic acid, useful for treatment, prevention, diagnosis and monitoring of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 318;
                                                                                                                                                                                                                                                                                                                          Th present invention relates to the isolation of novel cDNA
                                                                                                                                                                                                                                                                                                                                               encoding for at least an immunogenic portion of human colon
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16.1%; Score 184.8; DB 23; Length
Best Local Similarity 73.8%; Pred. No. 1e-38;
Matches 234; Conservative 0; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 318 BP; 76 A; 82 C; 83 G; 76 T; 1 other;
                                                                                                                                                                                                                                                                                    Claim 4; Page 246; 299pp; English
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                                 24-MAR-2000; 2000US-191597P.
04-MAY-2000; 2000US-202024P.
05-MAY-2000; 2000US-202189P.
                                                                                                                                                        King GE;
22-MAR-2001; 2001WO-US09246
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detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
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The sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profilling studies, in qualitatively quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries and sub-transcriptome under a libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 GATTGCCAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit a genome, useful for detecting tissue-, pathology-, and
       SS.
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oligonucleotide sequences from rats, humans and mice, whi
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splice variant; transcriptome; oligonucleotide library;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental-specific genes
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specification, but was
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les 60; Conserv
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                                                                          Homo sapiens.
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1 GATTGCCAACCAGTTCATGAGCAAGCAACTCCAGAACTACAGGTTCTTGTTGTGACC

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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 1.0
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AUTHORS TITLE	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BC014888	
Strausberg, R. Direct Submission	1 (bases 1 to 2577)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.	MGC.	BC014888.1 GI:15928849	BC014888	IMAGE: 3908026, mRNA, complete cds.	Homo sapiens, hypothetical protein P15-2, clone MGC:10178	BC014888 · 2577 bp mRNA linear PRI 29-OCT-2001		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.llr Series: IRAK Plate: 15 Row: c Column: 14 This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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REFERENCE KEYWORDS ORGANISM AUTHORS oligo capping; fis (full insert sequence). Homo sapiens ovary, tumor tissue cDNA to mRNA, clone:OVARC1000071. Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens AK023289 AK023289.1 GI:10435160 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., · Chordata; Primates; Craniata; Vertebrata; Catarrhini; Hominidae; Hominidae; Otsuki,T., clone_lib:OVARC1

AK023289 2692 bp Homo sapiens cDNA FLJ13227 fis, to Homo sapiens NTF2-related exp

sapiens

export protein

mRNA linear clone OVARC1000071,

r PRI 01-AUG-2002 71, weakly similar (NXT1) mRNA.

Nishikawa,T., Wagatsuma,M.,

Sudo, H.,

Suzuki,Y.,

Euteleostomi;

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Ishii,S., Kawai,Y., Saito,F
Nakamura,Y., Nagahari,K., N
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TLPEHTATRSQMATSLDFKTYYDQACRAAEEFVNIYYETMDKRRRALTRLYLDKATLI
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Direct Submission
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            CACTGTGAACCCAGCCTATTGCAAAAATAAAATCTTTTTATAATATTA
                                                           CATTCCACTAATGACATTCTTATAATAATATTAAACACATGATCTTGGTACTAACATACT
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                                                                                                                    GCCAGTTTGGAGCATTGCCCTCTAAGAGCTTTAAAAACTATTTTTTTACATGCCTTATATA
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                                                                                                                                                                                                                                                                                      AACTTCCTGCTGACTGCTCAGTCCACTCCCAACAATACTGTGTGGAAGATTGCAAGTGAT
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177 c 178 g 274 t
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/protein_id="AAF86878.1"
/db_xref="GI:9295188"
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/product="dJ596C15.1.1 (novel protein) (isoform 1)"
/product="march: ESTS AA23353 AA354023 AA333479 AA400543
/note="march: ESTS AA23353 AA354023 AA333479 AA400543
N27567 AA331754 AA459145 AA328722 R67870 H00878 AA148904
AA2335578 N20297 AA782964 AA400435 AA458927 AA525010
AI258152 AA234442 AA148905 AI066541 AI467944 R67871 R2567

R25673

complement (4444. 3683. .4070 /note="LlP

/note="L1PA5 repeat:

matches 4450. matches

.6143

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'note-

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'note="match: GSS

AQ132738"

/clone_lib="RPCI-4" /clone="RP4-596C15" /chromosome="X"

/organism="Homo sapiens" /db_xref="taxon:9606"

.17886

/note="L1P repeat: matches
complement(4444 . 12256)
/gene="dJ596C15.1"

complement(join(4444.

.6630,7518.

.7662,11006.

/gene="dJ596C

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REFERENCE AUTHORS
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HS596C15/c
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                                                                                                                                                                                                                                                                             requests: clonerequest@sanger.ac.uk

On Mar 24, 1999 this sequence version replaced gi:4464241.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence is the entire insert of clone 596C15. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An antempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS596C15 178863 bp DNA linear PRI 23-NOV-199 Human DNA sequence from clone 596C15 on chromosome xq23. Contains the GUCY2F gene for guanylate cyclase 2F, rethnal (EC 4.6.1.2, RETGC-2, Rod Outer Segment Membrane Guanylate Cyclase 2,4 ROS-GC2, GC-F) and a potentially alternatively spliced novel gene. Contains
                         596C15 is from the library RPCI4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-APR-1999) CB10 ISA, UK. E-mail end
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                                                                                                                                                     This sequence was generated from part of bacterial clone contig-
human chromosome X, constructed by the Sanger Centre Chromosome
Mapping Group. Further information can be found at
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gene="dJ596C15.1"</pre>
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7. .>11941))
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                                                                                                              ="L1M4 repeat:
. .17051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8821
.-"AluSg repeat: matches 4. .310 of consensus"
.10249
                                                    "L1MA9 repeat: matches
                                                                                     -"L1MA9 repeat: matches 5643.
                                                                                                                                                                                              "MIR repeat: matches
                                                                                                                                                                                                                                                                                                                        -"AluSg/x repeat: matches 134. .297 . .14229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -"MIR repeat: matches 37. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -"MIR repeat: matches 4.
                                                                                                                                                                                                                               ""L2 repeat: matches 2431. .2495 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                          -"L2 repeat: matches 2574. .2746 of consensus"
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                     repeat: matches 2176. . 2360 of consensus'
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ACTCCCAACAATACTGTGTGGAAGATTGCCAAGTGATTGCCTTTCCAGGATTGGTCT 574
                                                                        AAGTTTGATGGAAACAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCC
                                                                                                                                                          GTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTG
                                                  AAGTTTGATGGAAACAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCC
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                     /note="L1MB2 repeat: matches 5051. 35659. .36222
                                                                                                                                                                                                                                                                                                                     note="AluSx repeat: matches 22.
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1880..34949
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99.6%;
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L9. .20311
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:e="AluJo r
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9. .28661
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                                                                                                                                                                                             Score 747.2; DB 9;
Pred. No. 3.3e-159;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                     repeat: matches 1300.
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/tissue_type="testis"
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p15-2 gene; p15-2a protein.
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421 AGTAGTTAA 429
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ACTCCCAACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCT 6458
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                                      AGAGCTTTAAAAACTATTTTTTTACATGCCTTATATATACATTCCACTAATGACATTCTTATA
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                                                                           TATGTGAATTATTTTGATTGTAGAAGCACTATAATATGTGTGCTGAAACTAAATTTCTTTAA
                                                                                                                            TATTTTCTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Eurer
Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of p15, interacts with
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/db_xref="GI:8575520"
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/organism="Homo sapie
/db_xref="taxon:9606"
1. 429
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Eukaryota, Metazoa, Chordata,
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1 (bases 1 to 429)
Kang,Y. and Cullen,B.
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Unpublished
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Kang, Y. and Cullen, B.
Direct Submission
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TAP (NXFI) belongs to a multigene family of putative RNA export factors with a conserved modular architecture
Mol. Cell. Biol. 23, 8996-9008 (2000)

2 (bases 1 to 429)
Izaurralde,P.
                                                                                                                                                                                                                                                                                                                                                                                                                 215 TTTGTCAATATTTACTATGAGACAATGGATAAAAGAAGAGGGGCACTAACCAGGCTGTAT
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Catarrhini; Hominidae; Homo
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                                                                                                   Length 429;
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Submitted (26-APR-2000) Izaurralde E., Gene E
Meyerhofstrasse 1, 69117 Heidelberg, GERWANY
Related sequence: AJZ78323.
Location/Qualifiers
                                                                                                 37.4%; Score 429; DB 9; I
100.0%; Pred. No. 8.9e-87;
ive 0; Mismatches 0;
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Primates;
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/chromosome="X"
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                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 429;
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                                   1 (bases 1 to 567)
Herold,A., Suyama,M., Rodrigues,J.P., Braun,I.C., Kutay,U.,
Carmo-Fonseca,C., Bork,P. and Izaurralde,E.
TAP (NXF1) belongs to a multigene family of putative RNA export
factors with a conserved modular architecture
 Izaurralde, E.
                                                                                                                                  Homo.sapiens
                                                                                                                                                         AJ278323.1 GI:966:
p15-2 gene; p15-2b
                                                                                                                                                                                     Homo sapiens mRNA
AJ278323
                                                                                                         Eukaryota;
Mammalia; 1
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                                                                                                                                                                                                                                                                                                                                                                                  GTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTG
                                                                                                                                                                                                                                                                                             AGTAGTTAA 583
                                                                                                                                                                                                                                                                                                                                 ACTCCCAACATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCT
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            1. Cell. Biol. 23 (bases 1 to 567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MATSLDFKTYVDQACRAAEEFVNIYYETMDKRRRALTRLYLDKA
TLIWMGNAVSGLDALNNFFDTLPSSEFQVNMLDCQPVHEQATQSQTTVLVVTSGTVKF
DGNKQHFFNQNFLLTANGSTPNNTVMKIASDCFRFQDWSSS"
85 c 94 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNAs encoding for p15-2a
                                                                                                      Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=experimental
/product="p15-2a protein"
/protein_id="CAB96371.1"
/db_xref="CI:8920232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="the p15-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="p15-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'function="role in mRNA nuclear export"
                                                                                                                                                                       GI:9663146
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                        23, 8996-9008
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p15-2b
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Pred. No. 8.
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protein
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                        (2000)
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8.9e-87;
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in (P15-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
TGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAA 583
                                                              CAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCAACAATAC
                                                                                                                                                                                                                                                                     CTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTTGACAC
                                                                                                                                          AACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAA
                                                                                                                                                                                                                                                                                                                CTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCAC
                                                                                                                                                                                                                                                                                                                                               CTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                               GGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTTGCTGAGGAGTTTGTCAATATTTA
                                                                                                                        AACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAA
                                                                                                                                                                                                                   ATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATGAGCAAGC
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="VTNHVPALCTAGRGPREAARPAGPTPSLVSSRFLIPERTLSWEI
ARGGDVGDFKTVDQACRAAEDEVNIYYETMDKRRRALTRLYLDKATLLWNGNAVSGL
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LLTAQSTPNNTVWKIASDCERFQDWSSS"
131 c 142 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="role in mRN
/note="The p15-2 gene
mRNAs encoding for p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="p15-2b protein"
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/db_xref="G1:9663147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence-experimental
/product-"p15-2b prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P15-2"
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Pred. No. 1.3e-83;
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ene produces two alte
pl5-2a and pl5-2b pr
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Rattus norvegicus ***, 62 unordered

148320 bp DN norvegicus clone CH230-160A14, 2 unordered pieces.

DNA

SEQUENCING

linear

HTG 13-JUL-2002 S IN PROGRESS

AC107438

AC107438 AC107438.3 GI:21736312 HTG: HTGS_PHASE1.

Rattus norvegicus

REFERENCE AUTHORS

data html)

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Falls, T., Ferraguto, D., Flagg, M., Ford, J., Forter, P., Frantz, P., Falts, T., Ferraguto, D., Flagg, M., Ford, J., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Harris, K., Harris, M., Haylak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kireshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Moryan, M., Morris, S., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovłedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Prinus, E., Pu, L. L., Ouiles, M., Ren, Y., Rives, M., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Syatek, A., Tabor, P., Tamerisa, K., Tang, H., Sutton, A., Syatek, A., Tabor, T., Telfrod, B., Thomas, N., Thomas, S., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, D.M., Adams, C., Alsbrooks, S.L., Amara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 148320)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams,G., Williamson,A., Wieczyk,R., Wooden, Wu,C., Wu,Y., Zhou,J., Zorrilla,S., Ne Weinstock,G. and Globs,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18846336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
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Consensus quality: 94598 bases at least Q20 consensus quality: 98933 bases at least Q20
                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- project Information
Center project name: GMZC
Center clone name: CH230-160A14
                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Genome Center
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, Amaratunge,H.C., Are,J.R., Ayele,M., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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J., Chavez, D.,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'vorking draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                    AGTATTTAAAGGAGAAAAGCCCGT--TCGATTGGTCCATTAGTTCCAGCAAGAGAAGTT
                                                                                          ACTCCTAACAGCACGGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGGCT
                 TAATGTGAATTAATAGATTTCGTTGCAAAAGTACTATAAACTTAAGTGTATGTGCTAAAA
                                  TA----TGTGAATTATTTTGATTGTAGAAGCACTATAA----TATGTGCTGAAA
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VERSION KEYWORDS SOURCE REFERENCE ACCESSION DEFINITION LOCUS ORGANISM AUTHORS AC110357
Rattus norvegicus
***, 49 unordered Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus norvegicus HTG; HTGS_PHASE1. Rattus. AC110357.3 (bases 1 to 173939) norvegicus clone CH230-276M2, GI:21740885 pieces. 173939 ģ DNA linear SEQUENCING Euteleostomi;
; Murinae; HTG 13-JUL-2002 IN PROGRESS

ORS Muzny D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, K., Blankenburg, K., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bhlay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Delandy, C., Elan, J., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Edyardo, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Folgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Felagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hale, J., Jackson, L.E., Jackson, E., Kelly, S., Khan, U., King, L., Kovrah, J., Kovar, C., Kratovic, J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Luna, R., Martinez, E., Maher, G., Martinez, E., Matchell, T., Mohabbat, K., Morgan, M., Morris, S., Morsh, N., Newtson, J., Newtson, N., Newtson

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Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wieczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y., T., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced g1:18847131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
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Direct Submission
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Direct Submission
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Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
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Peters,L., Pickens,R., Primus,E
                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs: The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 136387 bases at least Q40
Consensus quality: 139690 bases at least Q30
Consensus quality: 142385 bases at least Q20
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GRMU
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                                                                                                                                                                                                                                               of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version re
                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Depar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                  Center: Baylor College of Center code: BCM
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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         575 AGTAGTTAAAAGGGGCAAAAGTCCATTCTCATTTGGTCCATTAGTTCCAGCAATTGAAATT 634
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corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least.
                                                                                                                           Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                   Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 21, 2002 this sequence version replaced gi:21955595.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
AL731672
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                                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
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one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em:, EMBL; Sw:, GRMPEP; Information on the WORMPEP
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                                                 AC-ATGCCTGTTTACGATTAACAC---
                                                                            ACGTTGCCTGTTTTCAGTTAACACTGGTAATGCCATTTTAATATATAGGCTTTTTTCAAATC
                                                                                                                                                                                ATATAACACTCTGGGAAGAAGTGGAGTTTTTTGGTTATTAGGTTAATTTTCTAGTAAAAC
                                                                                                                                                                                                                                                  AACCCGATCTATTGCACAAATGGAGTCCTTTTGTATTACTCTCTATGGGAT---AGCACA
                                                                                                                                                                                                                                                                            AACCCAGCCTATTGCAAAAATAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACA 917
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1. .232171
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Pred. No. 4.1e-52;
0; Mismatches 143;
                                                                                                                                                - AGGATAGTCTCAGTTACTAGGGTAATTTCTCAATGAAGC
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ACTTAGTTTTACGCTAGTGTTCTGACATATTTTAATTGC

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COMMENT
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Query Match
Best Local S
Matches 326
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TITLE
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 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web attention
                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G. Series: IRAL Plate: This clone was selec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 12 Row: m Column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Bendanin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S. Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R. Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 939)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC002687.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang, L.-H. and Green, E.D.
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IMAGE:3608037, mRNA, complete cds.
                    Similarity
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   Conservative
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                                                                                         /translation-"MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTAT
LVWNGNAVSGQESLSEFFEMLDSSEFQLSVVDCQPVHDEATPSQTTVLVVICGSVKFE
GNKQRDFNQNFILTAQASSPSNTVWKIASDCFRFQDWAS"
253 c 250 g 219 t
                                                                                                                                                                                                                                                                           /tissue_type="Uterus, endometrium adenocarcinoma"
/clone_lib="NIH_MGC_44"
/lab_host="DH10B-R"
                                                                                                                                                               /product="NTF2-related export
/protein_id="AAH02687.1"
/db_xref="GI:12803703"
                                                                                                                                                                                                                                                                                                                              /clone="MGC:3469 IMAGE:3608037"
                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"/db_xref="LocusID:29107"
                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         following selection criteria: matched mRNA g1: 7019470
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72.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.nisc.nih.gov/
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:
Score 251.6; DB 9;
Pred. No. 1.2e-46;
D; Mismatches 124;
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                  Clone distribution: MGC clone distribution
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                                                                                                                                                                                                     nfo@bcgsc.bc.ca
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162 CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA
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Janai: """

Tissue Procurement: ""

CDNA Library Preparation: Rubin """

CDNA Library Arrayed by: The I.M.A.G.E. Cor

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Conada
                                        Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (06-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Senomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Genomics O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens, NTF2-related export IMAGE:2820775, mRNA, complete and BCOLOGO
                                                                                                                                                                                                                                                                                                                              Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butter
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 963)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGGTGGCAGAGGTCTCTTTGCTTCATTC
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     Scott
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Zuyderduyn, Marco
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Erin Garland, Ran Guin,
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MGC:4329
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http://image.llnl.gov information can be found

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SOURCE
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Best Local Sin
Matches 326;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 965)
                                                       Homo
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                                                                                                                    Homo sapiens
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LVWNGRAVSGQESLSEFFEMLESSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFE
GNKQRDFNQNFILTAQASPSNYTYKIASDCFRFQDWAS"
263 c 256 g 224 t
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/protein_id="AAH03029.1"
/db_xref="GI:12804339"
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/clone_lib="NIH_MGC_7"
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              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 251.6; DB 9;
Pred. No. 1.2e-46;
0; Mismatches 124;
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d export
              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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342 TTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATG
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326; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUN-1999) Center Virginia, 7161 Hospital West, Charlottesville, VA 22908, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 96 Black, B.E. and Pa Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black, B.E., Levesque, L., Holaska, J.M., Wood, T.C. and Paschal, B.M. Identification of an NTF2-related factor that binds Ran-GTP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulates nuclear protein export
Mol. Cell. Biol. 19 (12), 8616-8624 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA 281
GGGGGTGGCAGAGGTCTCTTTGCTTCATTC
                                                                                             GCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGT
                                                                                                                                                                                                                                               ATGGAAACAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCA 521
                                                                                                                                                                                                                                                                                                ATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG
                                                                                                                                                                                                                                                                                                                                                 AGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTG
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                                              AAAGGGGCAAAAGTCCATTCTCATTTGGTC 611
                                                                                                                                            ACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTT 581
                                                                                                                                                                                                AGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCA
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LYWNCKAVSGGESLSEFFEMLESSEFQLSVVDCQPVHDEATPSQTTVLVVICGSVKFE
GNKQBDFNQNEILTAAQASPSNYTWKIASDCFRPQDWAS"
265 c 263 g 230 t
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/product="NTF2-related export protein
/protein_1d="AAD54942.1"
/db_xref="GI:5880865"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ran-GTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="stimulates nuclear protein export"
/note="similar to the sequence presented in GenBank
Accession Number AAA85905; nuclear transport factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"NXT1"
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odb_xref="taxon:9606"
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Pred. No. 1.2e-46;
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725
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Qу	Db 4			Query Match Best Local's Matches 32	BASE COUNT	CDS		FEATURES	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
42 TTGACACATTGCCTTCTAGTGAGTTCCCAGGTCAATATGTTAGATTGCCAACCAGTTCATG 401	202 ASSOCIACE INTERSPERANTS CONTROL 1	ATATTACTATIGACIACACIGGATAAAGAAGAGAGGCACTAACCAGGCTGTATCTGGACA	CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA	ch 22.0%; Score 251.6; DB 9; Length 972; 1 Similarity 72.4%; Pred. No. 1.2e-46; 326; Conservative 0; Mismatches 124; Indels 0; Gaps 0;	NO C	/cisue_type="Lung, small cell carcinoma" /clone_lib="NIH_MGC_7" /lab_host="DH10B-R" /note="Vector: pOTB7" 285 _ 707 /codon_start=1	rganism="Homo sapiens" b_xref="LocusID:29107" b_xref="taxon:9606" lone="MGC:2701 IMAGE:2820775"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: 1 Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 7019470. Location/Qualifiers	Ontact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan	g,R. gy,R. in to 972) gy,R. gy,R. in the state of the sta	BC000759 972 bp mRNA linear PRI 12-JUL-2001 HOMO Sapiens, NTF2-related export protein 1, clone MGC:2701 IMAGE:2820775, mRNA, complete cds. BC000759 BC000759.1 GI:12653930 MGC. HOMO Sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Search completed: June 28, 2003, 02:38:53 Job time: 3102.3 secs

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Result
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Maximum DB seq length: 2000000000
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                                                                   Score
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Match Length DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Alignment Scores:	PFGMI; PF02136; NTF2; 1. PFGMI; PF02136; NTF2; 1. SEQUENCE 200 AA; 23029 MW; B05E47D62B27B7FF CRC64;		O'Neil S., Harris D., Wood V., Rajandream M.A., Barrell B.G. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.	STRAIN-972H-;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=4896;	Schizosaccharomyces.	Schizosaccharomycetales; Schizosaccharomycetaceae;	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	Schizosaccharomyces pombe (Fission yeast).	SPAPB1A10.03.	Putative nuclear export factor.		01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	01-MAR-2001 (TrEMBLrel. 16, Created)	Q9HDY6;	Q9HDY6 PRELIMINARY; PRT; 200 AA.	IDY6	SULT 1
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01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 19.0 kDa protein.
Dictyostelium discordance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8T2G7
Q8T2G7;
                                                                                                                                                                                                                                                                                                Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and Analysis of Chromosome 2 of Dictyostellum."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC115607; AAL92371.1; ...
                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 167 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum
Eukaryota; Mycetozoa; Dic
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnilellelevalvalSerGlyThrileArgPheAspGlyLysLysProHisvalPhe
                             GAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTA
                                                                                AAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTC---AATATTTACTAT
ProLysTyrAspSerSerArgAlaAspLeuIleGlyLeuTyrLysAspHisSerValSer
                                                          LysLysIleValGluThrIleThrProArgAlaGluValPheIleLysGluPheTyrTyr
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                                                                                                                                                              4.92e-09
163.50
44.96%
31.01%
8.12%
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167.00
53.39%
27.97%
8.30%
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Dictyosteliida;

    SerAlaThrThrGlnProAspAspThrIlePheLys

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SEQUENCE 127 AA; 14317 MW; 2D45B1B20021B298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-AX4;
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Eukaryota; Mycetozoa; Dictyosteliida;
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                                                           ArgLysIleAsnSerIleAspCysGlnGlnThrTyr--
                                                                                                                     LeuSerGlyAlaAspAlaIleValLysHisIleValGluLeuProPheGlnGlnThrAsn
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 GlyIleMetIleThrValThrGlyThrLeuIleIleAspGlyGluAlaLys
                             ACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAACAACAACATTTCTTC
                                                                                         ArgAlaGlyLeuThrGlnIleTyrGlnGlnGlnThrThrLeuThrTrpGluGlyLysPhe
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150.00
46.83%
29.37%
7.45%
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     Q9P8H0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
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01-DEC-2001 (TrEMBLITE). 19,
01-MAR-2002 (TrEMBLITE). 20,
Nuclear transport factor 2.
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1-DEC-2001
1-MAR-2002
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                                                                          CGT
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                                                                                                                        CTGACTGCTCAGTCCACTCCCAACAATACT--
                                                                                                                                                                                                                                                                                                                   GCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACC
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                                                                                                                                                                                                LeuAspAlaGlnProSerGlyGluHisGly-
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                                                                                                                                               ValThrGlyAlaLeuLeuValAspGluGluLysAsn-
                                                                                                                                                                                                                      TTAGATTGCCAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTG
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   PRELIMINARY;
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127.50
47.11%
29.75%
6.33%
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Last annotation update)
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EMBL/GenBank/DDBJ databases
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                                 Q8RU32
Q8RU32;
Q1-JUN-2002
Q1-JUN-2002
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9P8H0;
01-OCT-2000
01-OCT-2000
01-JUN-2002
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Submitted (APR-2000) to the EM
EMBL; AF26031; AAF70316.1; -.
HSSP; P13662; 10UN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=4952;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Cordero Otero R.R., Lepingle A., Gaillardin C.
"RPHI gene from Yarrowla lipolytica.";
"RPHI gene from Yarrowla Lipolytica.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
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                       nuclear transport
                                                                                                                                  ProAspGlySerSerTyrTyrValPheAsnAspIlePheArg
                                                                                                                                                         CCCAACAATACTGTGGGAAGATTGCAAGTGATTGCTTCCGT
                                                                                                                                                                                  ValAspGlyAspAsnProLeuProTyrGlyGlnValPheHisLeu
                                                                                                                                                                                                        TTTGATGGAAACAAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACT
                                                                                                                                                                                                                                                       CATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAG
                                                                                                                                                                                                                                                                               ValGlyLeuProPheGlyGlnValArgHisLysIleSerAspIleAspAlaGlnProAla
                                                                                                                                                                                                                                                                                                     GACACATTGCCTTCTAGTGAG----
                                                                                                                                                                                                                                                                                                                                                    GCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTT
                                                                                                                                                                                                                                                                                                                                                                           PheTyrTyrGlnThrPheAspThrAspArgSerGlnLeuGlyAsnLeuTyrArgAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                         SerValAspPheAsnThr---
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                                                                                                                                                                                                                                 SerAlaGlnGlyGlyAsp--
                                                                                                                                                                                                                                                                                                                             SerMetLeuThrPheThrGlyThrGlnH1sGlnGlyAlaGlnAlaIleValGluLysLeu
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                                 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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 (japonica
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121.50
44.78%
27.61%
6.04%
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cultivar-group)
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21,
                                   Last sequence u
                                                            Created)
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EMBL/GenBank/DDBJ
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                                                                                  PRT;
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Matches:
Conservative:
Mismatches:
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                                                                                  146
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Best Local Similarity:
                                                                                                                                                                                                                                                                          Q917J5
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"Oryza sativa (japonica cultivar-group) genomic DNA, chi
clone:P0415A04.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AP003345; BAB90110.1;
SEQUENCE 146 AA; 15796 MW; 496BE9A02E1E9670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidese; Oryzeae; Oryza.
NCBI_TaxID-39947;
                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
                                                                                                                                                                        Rin protein
RIN OR CG94
  Adams M.D., Celniker S.E., Holt R
Amanatidės P.G., Scherer S.E., Li
George R.A., Lewis S.E., Richards
                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                           MEDLINE=20196006; PubMed=10731132;
                                                                       SEQUENCE FROM N.A.
                                                                                                Ephydroidea; Dro
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                AAGATTGCAAGTGATTGCTTCCGT 559
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120.00
44.53%
30.47%
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16,
21,
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Last annotation update)
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R.A., Evans C.A.,
Li P.W., Hoskins R.
ds S., Ashburner M.
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 R.A., Galle R.
M., Henderson
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59
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              Galle R.
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Best Local Similarity:
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Ak Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreff A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson K.A.,

Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Y.H., Zhong F.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM;
SEQUENCE 688 AA. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutton G.G.,
Brandon R.C.
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InterPro; IPR002075; NTF2.
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EMBL; AE003701; AAG22151.1; -.
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                                      ATGTTAGATTGC--
                                                                                                                             GlyGlnArgGluIleHisAsnArgIleGln----
                                                                                                                                                                                                           GGGCTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAAT
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Bouck J., Brokstein P., Brottier
Butler H., Cadieu E., Center A., C
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., Champe M., Pfeiffer B.D.,
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X.; Smith H.O.
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RESULT 8
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Best Local Similarity:
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EMBL; AF231031; AAF68949.1; -.

FlyBase; FBgn0015778; rin.

InterPro; IPR002075; NTTT
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                   ATGTTAGATTGC
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                                                                                                     GGGCTGGATGCCCTAAATAATTTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAAT 376
                                                                                                                                          LeuHisArgPheTyrAsnHisAsnSerSerTyrIleHisGlyGluSerLysLeuValVal
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RA RA RA RA RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly),
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000
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Beeson K.Y., Benos P.\
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                                                                                                                                            Yeh R.-F., Zaveri J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benos P.V., Berman B.P., Bhandari D., Bolshakov
Botchan M.R., Bouck J., Brokstein P., Brottier P.
Busam D.A., Butler H., Cadieu E., Center A., Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delniker S.E., Holt R.A., Evans C.A., G.G., Scherer S.E., Li P.W., Hoskins R.A. Lewis S.E., Richards S., Ashburner M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                   Zhong W., Zhou X., Zhu
Rubin G.M., Venter J.C.
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Last annotation update)
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                                                                                                                  Zhan M., Zhang G., Zhao Q.,
Zhou X., Zhu S., Zhu X.,
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                                                                                                                                                           Yang S., Yao Q.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insecta;
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                                                                                                                                                                                                    Wang X.
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Smith
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01-OCT-2000
01-OCT-2000
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Champe M., Chavez C., Dorsett V., Farran, Champe M., Chavez C., Dorsett V., Farran Gonzalez M., Guarin H., Li P., Liao G., Miranda Gunzalez M., Gacleb J., Paragas V., Park S., Phouar Nunco J., Pacleb J., Rubin G.M., Celniker S.;
Vu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                   01-JUN-2002
T23J18.22.
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EMBL; AP003701; AAF54965.1; -.
EMBL; AY058617; AAL13846.1; -.
FlyBase; FBgn0015778; rin.
InterPro; IPR002075; NTF2.
InterPro; IPR002075; NTF2.
Ffam; PF00136; NTF2; 1.
Pfam; PF02136; NTF2; 1.
SMART; SM00360; RRM; 1.
                                 Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                 Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                AGTGATTGCTTCCGTTTTCAAGAT
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                                                                                                                                                                                                                                                                                                                ThrGlnThrPheValLeuAlaAlaGlnSerProLysLys-.
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                                                                                                                                (TrEMBLrel.
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                                                                                                                 (TrEMBLrel.
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tt V., Farfan D., Frise
                                                                                                                                                                                   PRT;
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Matches: Conservative: 
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63
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                                                  eudicots;
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ngall C.J.,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TremBLrel. 21, Last annotation update)
           Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L. Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Le Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri
                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                              NCBI_TaxID=3702;
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HSSP; P13662; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis Ecker J.R.;
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                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                F17L21.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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nm P., Sakano
Vaysberg M.,
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 Federspiel N.A.,
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endopterygota;
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17,
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Last annotation updat
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US-09-763-902B-15 (1-1146) x Q9VJ85
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Best Local Similarity:
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Q9SFV5;
01-MAY-2000 (TrEMBLrel. 13, C)
01-MAY-2000 (TrEMBLrel. 13, La
01-JUN-2002 (TrEMBLrel. 21, La
Putative RNA-binding protein.
                STRAIN-CV. COLUMBIA:
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T1B9 genomic sequer
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC012395; AAF20221.1;
                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
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SEQUENCE 130 AA; 145
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Gibbs
"The g
                                                                                                                                EQUENCE FROM N.A.
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Science 287:2185-2195(2000)
EMBL; AE003659; AEF53669.1; -.
HSSP: P13662; 10UN.
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R.A., Myers E.W.,
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Last annotation update)
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Matches:
Conservative:
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Indels:
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databases;
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DB:
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Best Local Similarity:
STRAIN-BRISTOL N2;
Macri C., Vaudin M.;
"The sequence of C. e
Submitted (MAR-1999)
[3]
                                                                                                                                                                                                                                                                                                          095YF0;
01-DEC-2001 (
01-DEC-2001 (
01-JUN-2002
                                                                                                "Genome sequence of the nematode investigating biology. The C. elescience 282:2012-2018(1998).
                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE-99069613;
                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Hypothetical 153.1 kDa |
                                                                                                                                                                                                                                                                                                                                                                       Q95YF0
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=6239;
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PROSITE; PS50102; RRM; 2.
SEQUENCE 946 AA; 105623
                                                                                                                                                                                       EQUENCE FROM N.A.
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                                                                                                                                                          PubMed=9851916;
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          cosmid C07H6.";
EMBL/GenBank/DDBJ
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                                                                                                              Consortium.";
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submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; AC006605; AAK85441.2;
Interpro; IPR000357; HEAT_repeat.
PROSITE; PS50077; HEAT_REPEAT; 1.
Hypothetical protein.
SEQUENCE 1378 AA; 153109 MW; E2DA7981417FU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston
SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916;
                                                                                                   Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                   Submitted (JAN-1996)
                                                                                                                            Caenorhabditis elegans
                                                  Hembry
                                                                                    CBI_TaxID=6239;
                                                                                                                                                                   )1-NOV-1996
)1-NOV-1996
)1-JUN-2002
                                                              EQUENCE FROM N.A.
                                                                                                                                                     08F4.2 protein
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Science 282:2012-201
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Search completed: June 24, 2003, 19:36:59
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Result
No.
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-Q-/cgn2_1/USPTO_spool/US09763902/runat_24062003_130340_12418/app_query.fasta_1.2254
-Q-/cgn2_1/USPTO_spool/US09763902/runat_p.rsp -MINMATCH=0.1 -LOOPCL=0
-DB-SwissProt_40 -OPMT=-fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEX=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-NODE=-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09763902_eCGN_1_146_erunat_24062003_130340_12418 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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     TISSUE-Ovarian carcinoma;
TISSUE-Ovarian carcinoma;
TISSUE-Ovarian carcinoma;
TISOgai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kono Y., Takiguchi
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NXT2_HUMAN STANDARD; PRT; 142.AA.

G9NRJB; G9HBUO; G9NRLT; G9Y3M4; G9Y3M5; G9NQ64

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

NTF2-related export protein 2 (p15-2 protein)
                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
L1 Y., Peng Y., Li N., Gu W., Han Z., Fu G., Chen
"Novel genes expressed in human dentritic cell.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                       MEDLINE=20528640; PubMed=11073998;
Herold A., Suyama M., Rodrigues J.P., Braun I.
Carmo-Fonseca C., Bork P., Izaurralde E.,
"TAP (NXF1) belongs to a multigene family of p
factors with a conserved modular architecture.
Mol. Cell. Biol. 23:8996-9008(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                         Kang Y., Cullen B.;
"p15-2, a homologous
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM
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                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
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YKU5_CAEEL
RA13_SCHPO
VP43_NPVAC
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SIBA_MOUSE
G3BP_SCHPO
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ACHX_HUMAN
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CKAA_BACUF
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ARH6_HUMAN
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Q9Y3M5; Q9NQ64;
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                                                                                                                                                                                                                                                                                                                                           of putative RNA export ture.";
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modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1 AND
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European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Regulator of protein export for Also plays a role in mRNA nuclear export SUBUNIT: Associates with NXF1, NXF2, NXF3 SUBCELLULAR LOCATION: Nuclear Shuttles b
                                                                                                                                                                                                                                                                                                                                                                    AJ277591; CAB96371.1;
AJ278332; CAC01129:1;
AF246127; AAF78034.1;
AF201942; AAF86878.1;
AK023289; BAB14511.1;
AK023289; BAB14511.1;
AK023289; CAB41301.1;
AL031387; CAB41302.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: 2 isoforms; A produced by alternative splicing. SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Regulator
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02136; NTF2; 1.
PS50177; NTF2_DOMAIN; 1.
t; Protein transport; mRNA transport; Nuclear protein;
                                                                                                                     gene
TTTGTCAATATTTACTATGAGACAATGGATAAAAGAAGACGGCACTAACCAGGCTGTAT
                                                            CTGGACAAGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAAT
                                        PheValAsnIleTyrTyrGluThrMetAspLysArgArgAlaLeuThrArgLeuTyr
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EMBL/GenBank/DDBJ databases
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aitawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aitawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aitawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
RA Sakai K., Okido T., Fletcher C., Fujita M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QZV9; Q9D1P7;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
This SWISS-PF
between the
the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20036817; PubMed=10567585;
Black B.E., Levesque L., Holaska J.M., Wood T.C., Paschal B.M.;
"Identification of an NTF2-related factor that binds Ran-GTP and regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
NXT1_MOUSE
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                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21085660;
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                                                                                                                                                                                                                                                                                                                                                                      'Functional annotation
                                                                                                                                                                                                                     FUNCTION: Stimulator of protein proteins. Also plays a role in tRNA, and mRNA (By similarity) SUBUNIT: Preferentially binds
                                                                                                                                                                        and NXF3.
SUBCELLULAR LOCATION:
SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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'6J; TISSUE-Embryo;
5660; PubMed-11217851;
chibata K.
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                                                                                                                                                                                                                                                                                  of protein export for NES-containing a role in the nuclear export of Ul snRNA,
                                                                                                                                                                        Nuclear.
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Sciurognathi; Muridae
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                                                      a collaboration
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outstation -
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US-09-763-902B-15
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or send a
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        Black B.E., Levesque L., "Identification of an NT
                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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                           SEQUENCE FROM N.A.,
MEDLINE=20036817; P
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L5-JUN-2002
                                                                                                                                             6-OCT-2001
                                                                                                                                                                  _HUMAN
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PF02136; NTF2; 1.
TE; PS50177; NTF2_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                   AATACTGTGTGGAAGATTGCAAGTGATTGCTTTCCGTTTTCAAGATTGGTCTAGT
                                                                                                                                                                                                                                                 GGAAACAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCAAC
                                                                                                                                                                                                                                                                                           AspAlaThrProSerGlnThrThrValLeuValValIleCysGlyThrValLysPheGlu
                                                                                                                                                                                                                                                                                                                 CAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTCACCAGTGGAACTGTGAAGTTTGAT
                                                                                                                                                                                                                                                                                                                                                         GACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATGAG
                                                                                                                                                                                                                                                                                                                                                                            AlaThrLeuValTrpAsnGlyAsnAlaValSerGlyGlnGluSerLeuSerGluPhePhe
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
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                  Pubmed=10567585;
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protein export.";
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Catarrhini;
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RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Coulson A., Coville G.J., Deadman R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Huckle E., Hunt A.R., King A., Knights A., Laird G.K., Lawlor S.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Milme S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Kuce C.D., Smith M.L., Soderlind C., Steward C.A., Sulston J.E.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
               EMBL;
                                                                                                                                                             rnis SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guzik B.W., Levesque L., Prasad S., Paschal B.M., Rekosh D., Hammarskjo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ossareh-Nazari
Dargemont C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Cell. Biol. [2]
                                                                                                           modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                              the cytoplasm.
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                                                     EMBL;

    -!- SUBCELLULAR LOCATION: Nuclear.

                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Stimulator of protein export
proteins. Also plays a role in the nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21160285; PubMed=11259602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               classes of RNA in
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Mol. Cell. Biol. 21:2545-2554(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                        "NXT1 (p15) is a crucial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "RanGTP-binding protein
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AF156957; AAD54942.1;
AL096677; CAC03437.2;
BC000759; AAH00759.1;
BC0002687; AAH02687.1;
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414:865-871(2001)
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Barlow K.F., Bates K.N., Beard
P., Bird C.P., Blakey S.E., Brid
                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
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Hammarskjold M.L.;
cellular cofactor in
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Bentley D.R., Beck S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport;
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                                                                                                            Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                            NXT1_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
 SEQUENCE FROM N.A. STRAIN-Berkeley;
                                                    SEQUENCE FROM N.A.
MEDLINE=20036817; PubMed=10567585;
Black B.E., Levesque L., Holaska J
"Identification of an NTF2-related
                                                                                                                                                           Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                   NTF2-related
                                                                                                                                                                                                                                  Q9V3H8;
                                                                                                                                                                                                                                                        DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
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BC003410; AAH03410.1;
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ear protein export.";
l. 19:8616-8624(1999).
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

4.15e-25 310.00 60.90% 42.86% 15.40%

Length: Matches: Mismatches: Conservative: Indels:

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AA;

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Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X., RA Liu X., Mattei B. McIntosh T.C., McLeod M.P., McPherson D., RA Liu X., Mattei B. McIntosh T.C., McLeod M.P., McPherson D. L., Ra Mcunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra McIson D.R., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang S.-Y., Woddse T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra, Mallians S.M., Woodse T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra, Zheng X.H., Zhong F.N., Zhong W., Zhon G., Zheng L., Ra Zheng R.A., Myers E.W., Rubin G.M., Venter J.C., Through S.M., Schence 287,2185-2195(2000).
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Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
Transport;
                                                           Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN;
                                                                                                                       FlyBase; FBgn0028411; Nxtl.
InterPro; IPR002075; NTF2.
                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sibor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Stimulator of protein export for proteins. Also plays a role in the nuclear tRNA, and mRNA (By similarity).
-!- SUBUNIT: Preferentially binds Ran-GTP (By s
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between
the Euro
 EMBL;
EMBL;
HSSP;
                                           the European Bioinformatics Institute.
use by non-profit institutions as lo
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entitles requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                  Bradshaw-Cordum H., Scott K., Graves T.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: Stimulator of protein export for NES-contain proteins. Also plays a role in the nuclear export of tRNA; and mRNA (By similarity).
-I-SUBUNIT: Preferentially binds Ran-GTP (By similarity).
-I-SUBCELLOUAR LOCATION: Nuclear (By similarity).
-I-SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                   MEDITIE=20036817; PubMed=10567585; Black B.E., Levesque L., Holaska J.M., Black B.E., Levesque I., Holaska J.M., "Identification of an NTF2-related fact regulates nuclear protein export.", Mol. Cell. Biol. 19:8616-8624(1999).
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Rhabditidae; Pelode
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                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restiby non-profit institutions as long as its content fied and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                    Peloderinae;
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    Last sequence update)
    Last annotation update

                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                                                                 Nematoda;
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                                                        (See http://www
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                                                                                                                                                                                                                                                                                              Wood T.C., Paschal B.M.;
tor that binds Ran-GTP an
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                                                          .isb-sib
                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                 Rhabditoidea;
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NTF2_ORYSA
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                                                                                                                                                                                                                                                                     NTF2_ORYSA
Q9XJ54;
                                                                                                                                                            Spermatophyta;
Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport;
DOMAIN
                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                       Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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16-0CT-2001
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SQ FIRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
STRAIN-cv. Nipponbare;
Matsuki R.; Iwasaki T.,
"Molecular cloning of a
(NTF2) from rice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02136; NTF2; PROSITE; PS50177; NT
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; Y71F9AM.5;
                                                                                     (NTF2) from rice
                                                                                                                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                 LeuProGluGlyValThrGlyAspMetSerGlyGlyMetLeuLeuAsnValAlaGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCATGAGCAAGCAACTCAGTCCCAAACT---ACAGTTCTTGTTGTGACCAGTGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluPheMetLysAlaLeuProSerThrGlnHisAspIleGlnSerLeuAspAlaGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetLysThrThrGlnGluIleAsnLysGluAspGluGluLeuCysAsnGluSerLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGAAGTTTGATGGAAACAAACAATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAG
                                                                                                                                                                                                                   Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                              (Rel. 40, Las
(Rel. 40, Las
insport factor
                                                                                                                                                                                                                                 (Rice)
                                                                                                                                                                                      Magnoliophyta;
Oryzeae; Oryza
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                                                                                                                                                                                                                                                                                                                                       STANDARD;
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207.50
54.68%
29.50%
10.31%
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Last annotation
tor 2 (NTF-2).
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ctor 2
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                                                                                                  Jiang
cDNA e
                                                                                                                                                                                                                   Streptophyta;
                                                                                                  ng C., Yama
A encoding
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                                                                                                                                                                                                    Liliopsida;
                                                                                                                                                                                                                                                                                                                                       PRT;
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Conservative:
Mismatches:
Indels:
                                                                                                  Yamamoto N.;
ling nuclear
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                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
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                                                                                                                                                                                                     Poales;
                                                                                                    transport
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                              SIMILARITY)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606, 10090, 10116;
                                                                                                                  NTF2
                                                                                                                          01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear transport factor 2 (NTF-2) (Placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport;
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                                                                                       Mus musculus
                                                                                                                                          01-JAN-1990
15-JUN-2002
                                                                                                                                                                     01-JAN-1990
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            SEQUENCE FROM N.A
                                                                                                                                                                                              NTF2_HUMAN
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P13662; lA
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                                                                                                                                                                                                                                                                                                                                                                                                       ValAspCysGlnPro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAG-----TTCCAGGTCAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                TTAGATTGCCAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaLysAlaPheValGluHisTyrTyrArgThrPheAspThrAsnArgProAlaLeuVal
                                                                                                                                                                                                                                                                                                  Phe---
                                                                                                                                                                                                                                                                                                                         TTCCTGCTGACTGCTCAGTCCACTCCCAACAATACTGTGTGGAAGATTGCAAGTGATTGC 553
                                                                                                                                                                                                                                                PheArg 118
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                                                                                      (Mouse),
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A
                                                                                                                                                                                               STANDARD;
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124.00
47.54%
31.97%
6.16%
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84100EBB62AB1BD1
                                                Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                               PRT;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                               127
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                                                                                                                                                                                                                                                                                                                                                                                                     -SerGlyProGlnGlyGlyMetLeuValPhe
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                                                 Hominidae;
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                                                               Euteleostomi,
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Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A., Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatau N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shihagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grundmann U., Nerlich C., Rein T., Lottspeid "Isolation of cDNA coding for the placental Nucleic Acids Res. 16:4721-4721(1988).
Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-Human, and
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Gerace L., Silver P.A., Stewart M.;
"Nuclear protein import is decreased i
transport factor 2 (NTF2) that do not
J. Mol. Biol. 272:716-730(1997).
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                                                                                                                                                                                                                              Stewart M., Kent H.M., McCoy A.J.;
"Structural basis for molecular recognition between nucle
factor 2 (NTF2) and the GDP-bound form of the Ras-family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-98035028; PubMed-9368653;
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Bullock T.L., Clarkson W.D., Kent
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EMBL;
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01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Probable nuclear transport factor 2 (NTF-2)
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                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                   SEQUENCE
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PROSITE; PS50177; NTF2_DOMAIN; 1.
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   206
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P13662; 1A2K.
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J., Peat N., Hayles J., Baker S., Basham D., Bowman
, Brown D., Brown S., Chillingworth T., Churcher C.
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A Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Chung P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Chun P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

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A Chun P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., B., Kwan A., Liam B.,

A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Militscher J., Miranda M., Nguyen M., Romey T., Rowley D.,

B A Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
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Eukaryota; Viridiplantae; Streptophyta;
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                                                                                                          FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                               European Bioinformatics Institute.
                                                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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STRAIN-BD-A / FGSC 1858;
Meyer U., Meyer M., Techel D., Toeken K., Rensing L.;
Meyer U., Meyer M., Techel D., Toeken K., Rensing L.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: FACILITATES PROTEIN: TRANSPORT INTO THE NUCLEUS.
-PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT
AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY)
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
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                                                                                 Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
Amphibia; Batrachia; Anura; Mesobatr
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                           SEQUENCE FROM N.A.
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PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                      CBI_TaxID=8355;
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ae; Xenopus
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-1- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.

INTERACTS WITH THE NUCLEOPORIN PS AND WITH RAN. ACTS AT A RELATIVELY LATE STAGE OF NUCLEAR PROTEIN IMPORT, SUBSEQUENT TO THE INITIAL DOCKING OF NUCLEAR IMPORT LIGAND AT THE NUCLEAR ENVELOPE. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THE ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY
                                                                                                         Q9P926;
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the European Bioinformatics Institute
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   Eukaryota;
                Candida albicans (Yeast)
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PROSITE; PS50177; NTF2_DOMAIN;
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                                             Nuclear transport
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RESULT 13
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                                                                                                                                                                                                                                                                  GluLysLeuAlaSerLeuProPheGlnLysValAlaHisArgIleSerThrLeuAspAla
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                                                                                                                      GluLeuLeuIleAspGluGluGlnAsnAlaGlnArg
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                                                   -IleProAspAsnGlySerTyrTyrValPheAsnAspIlePheArg 120
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US-09-763-902B-15 (1-1146) x NTF2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E.,
Dietrich F.S., Mulligan J.T., Carpenter J., Chen E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomyce
Saccharomycetaceae; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-84 FROM N.A. Haarer B.K., Petzold A.S., Brown S.S.; Submitted (JUL-1993) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear transport
NTF2 OR YER009W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTS WITH VARIOUS NUCLEOPORIUS AND WITH RAN-GDP. COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT. IN VITRO, THE NTF2-RAN-GDP ASSOCIATION, IN THE PRESENCE OF GTP, TRIGGERS DISSOCIATION OF THE KARYOPHERIN ALPHA-BETA COMPLEX, ALLOWING NUCLEAR TRANSLOCATION OF KARYOPHERIN ALPHA AND THE NLS SUBSTRATE.

-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U18778; AAB64542.1; -. EMBL; L22204; AAB49379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 272:120-122(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                  Transport; Protein transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
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S0000811; NTF2
                                                                                                                                                                                                                                                                                            Scores:
                                                                                                                                            Similarity:
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                                                               Alignment Scores
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
-I- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.
-PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT
AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY)
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                               EMBL; 275546;
HSSP; P13662;
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                  Transport; Protein DOMAIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                        nterPro; IPR002075; NTF2.
%am; PF02136; NTF2; 1.
ROSITE; PS50177; NTF2_DOMAIN; 1.
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                                                                                                                                                                                                                                             VormPep; R05D11.
                                                                                                                                                                                                                                                                                                                               or send an
                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kennedy D., Mattick J.S.;
"Characterisation and chromosomal location members of a novel SH3 domain-binding and Fimplicated in signal transduction.";
Submitted (APR-1999) to the EMBL/GenBank/DI
SEQUENCE FROM N.A.
                                                                    Guitard
                                                                                                                                                                                        "Prediction of the coding sequences of The complete sequences of 100 new cDNA
                                                                                                                                                                                                                                    Ishikawa K.-I., Nagase T., Suya
Kotani H., Nomura N., Ohara O.;
                                                                                      rissue-Brain;
                                                                                                                                                                                                                                                                                                           TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS A AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                 MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                         EQUENCE FROM N.A.
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                                                                                                                                                    large proteins in vitro. 5:169-176(1998).
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                                         (FEB-1998) to the EMBL/GenBank/DDBJ databases
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ArgProAsnAsnGlnGlySerTyrPhe 120
                                                                                                                                                                                                                                                                                                                                                                                                        n of G3BP-1 and G3BP-2a/b, RNA-binding protein famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-763-902B-15 (1-1146) x G3B2_HUMAN (1-482)
                                                                                                                            Alignment Scores: Pred. No.:
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF145284; AAD51932.1; -.
EMBL; BA014560; BAA31635.1; -.
EMBL; AF051311; AAC15705.1; -.
EMBL; AF053535; AAC95292.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH IKAPPABALPHA. MEDLINE-20549669; PubMed-10969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
Kennedy D., Ru K., Mattick J.S.;
Submitted (MAR-1998) to the EMBL
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00076; rrm; 1.
Pfam; PF02136; NTF2; 1
SMART; SM00360; RRM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as lon modified and this statement is not remov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rigent M., Barlat I., Langen H., Dargemont C.;
IkappaBalpha and IkappaBalpha /NF-kappa B complexes are retained
the cytoplasm through interaction with a novel partner, RasGAP
                                                                                                                                                                                                                                                                        NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISSP; P09651;
                                                                                                                                                                                                                                                                                                                                                                                                   ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B;
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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SUBUNIT: BINDS TO THE N-TERMINAL DOMAIN OF IKAPPABALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED IN MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch)
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419
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482 AA;
                                                                                                                                                                                                                                                                                                                               -binding; Alternative splicing.
1 133 NTF2.
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                                                                                                                                                                                                                                                    MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                           GLU-RICH
                                                                                                                                                                                                                                                                                                       RNA-BINDING (RRM).
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Matches:
Conservative:
Mismatches:
Indels:
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V (IN REF. 3).
I (IN REF. 3).
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GluPheValArgGlnTyrTyrThrLeuLeuAsnLysAlaProGluTyrLeuHisArgPhe 33 GAGTTTGTCAATATTTACTÄTGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTG

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PheArgTyrGluAsp 135
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                                                                                  ValLeuAlaProGluGlySerValProAsnLys---
                                                                                  PheTyrValHisAsnAspMet 130
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112

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Search completed: June 24, Job time: 21.3988 secs 2003, 19:32:13

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R;Grundmann, U.; Nerlich, C.; Rein, T.; Lottspeich, F.; Kuepper, H.A. Nucleic Acids Res. 16, 4721, 1988
A;Title: Isolation of cDNA coding for the placental protein 15 (PP15). A;Reference number: S00751; MUID:88247772; PMID:3380696
A;Accession: S00751
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A; Residues: 1-127 <GRU>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo saptens (man)
C;Date: 31-Dec-1988 *sequence_revision 31-Dec-1988 *text_change 24-Sep-1999
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N;Alternate names: PP15
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                                                                                                                                  215 TTTGTCAATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTAT
                                                                                                        54 GluLysLeuSerSerLeuProPheGlnLysIleGlnHisSerIleThrAlaGlnAspHis 73
                                                    34 IleAspAlaSerCysLeuThrTrpGluGlyGlnGlnPheGlnGlyLysAlaAlaIleVal 53
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Sequence:

Qy 497 CTGCTGACTGCTCAGTCCACTCCCAACAATACTGTGTGGAAGATTGCAAGTGATTGCTTC 556	83 ValThrGlyGluLeuLeuAspGluGluGlnMetAlaGlnArgTyrSerGlnValPhe 10	QY 440 ACCAGTGGAACTGTGAAGTTTGATGGAAACAAACAACATTTCTTCAACCAGAACTTC 496	Oy 380 TTAGATTGCCAACCAGTTCATGAGCAAGCTAGTCCCAAACCTACAGTTCTTGTTGTG 439	Qy 326 GCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATG 379 :::	266 AGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGA	206 GCTGAGGAGTTTGTCAATATTT 	5.61% Indels: 2 Gaps: 146) x T38039 (1-123)	Alignment Scores: 0.00124 Length: 123 Pred. No.: 113.00 Matches: 34 Percent Similarity: 47.93% Conservative: 24 Best Local Similarity: 28.10% Mismatches: 51	superfamily: yeast n	197; PIDN:CAA9238(Reference number: 221740 Reference number: 221740 Reference number: 737728	: 1-123 (MCD> ferences: EMBL:AL109951; P fital source: strain 972h; K:; Churcher, C.M.; Barrel fo the BMRT, Data Tibrary	A;Accession: T38039 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	McDougall, R.C.; Raubmitted to the EMBI	C; Accession: T38039; T37728		Oy 509 CAGTCCACTCCCAACAATACTGTGTGGAAGATTGGAAGTGATTGCTTCCGT 559	Db 88 GlnLeuLysAlaAspGluAspProlleMetGlyPheHisGlnMetPheLeuLeu 105	ACTGTGAAGTTTGATGGAAACAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCT		
н86248	SULT 4	Qy 55/ CGT 559		QY 40 ACCASTGGAACTSTGAAGTTTGATTTGAACAACAACATTTC **TICAACCAGAACTTC 450	380 TTAGATTGCCAACCAGTTCATGAGCAAGCTAGTCCCAAACTACAGTTCTTGTTGTG ::: 70 ValAspCysGlnProserGlyProAlaserGlyMetLeuValPhe	Qy 326 GCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATG 379 :::::: :::! Db 50 SerIleValAlaLysLeuThrSerLeuProPheGlnGlnCysLysHisHisIleSerThr 69	Qy 266 AGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGA	206 GCTGAGGAGTTTGTCAATATTT 	US-09-763-902B-15 (1-1146) x B86405 (1-126)	Alignment Scores: Pred. No.: 10.00141 Score: 112.50 Percent Similarity: 47.93% Best Local Similarity: 27.77% Ouery Match: 2.59% Gaps: 126 Matches: 2.59% Conservative: 25 Mismatches: 52 Gaps: 5	A;Map position: 1 C;Superfamily: yeast nuclear transport factor NTF2	Status Molecu Residu Cross	A:Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A:Accession: B86405	izzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;	Aisen, W.F.; huykes, B.; huzzar, E.; Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.: Li, J.H.: Li, Y.; Lin, X.: Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia	, , ,	probable nuclear transport factor 2 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accesión: BEA/05	RESULT 3	 119 Arg	557 CGT 559	

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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
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ansen, N.F.; Hughes, B.; Huizar,
Nature 408, 816-820, 2000
                    A; Authors: Salzberg, S.L.;
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Date: 02-Mar-2001 #sequence_revision
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                                                                                                                           Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:AE005172; NID:g6554189; PIDN:AAF16635.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
Cross-references: EMBL:L22204; NID:g347714; PIDN:AAB49379.1;
                                                                                                                                                                                                                                                                                Dietrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: F17L21.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
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A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: H86398 A;Status: preliminary
A; Reference number: S41793
A; Accession: S41793
                                                                                                    A;Molecule type: DNA
A;Residues: 1-125 <DIE>
A;Cross-references: EMBL:U18778; NID:g603592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
C; Superfamily: yeast nuclear
                                         submitted to the EMBL Data Library, A; Description: Identification of mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-763-902B-15 (1-1146) x H86398 (1-122)
                                                                                  R; Haarer, B.K.; Petzold, A.S.; Brown,
                                                                                                                                                                                           submitted to the EMBL Data Library, A;Description: The sequence of S. coa;Reference number: S50459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005172; NID:g9802547; PIDN:AAF99749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA 
A;Residues: 1-122 <STO>
                                                                                                                                                                   A; Accession: S50467
                                                                                                                                                                                         Reference number:
                                                                                                                                                                                                                                                                                                                                       N; Alternate names: protein YER009w
                                                                                                                                                                                                                                                                                                                                                               nuclear transport factor NTF2 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                            ;Species: Saccharomyces cerevisiae;Date: 28-Jan-1995 #sequence_revision;Accession: S50467; S41793; S72237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 GCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCCGT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValSerGlyAsnLeuGlnLeuAlaGly---GluGlnHisAlaLeuLysPheSerGlnMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAGTGGAACTGTGAAGTTTGATGGAAACAAACAACATTTC----TTCAACCAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTTGAGTTCCAGGTCAATATG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaLysAlaPheValGluHisTyrTyrSerThrPheAspAlaAsnArgProGlyLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTÄGATTGCCAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerLeuTyrGlnGluGlySerMetLeuThrPheGluGlyGlnLysIleGlnGlySerGln 46
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Indels:
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                                                                                                                                                                                                                 cosmids
                                                                                                        PIDN: AAB64542.1;
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                                         synthetically
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36
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52
14
                                                                                                      PID:g603601;
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                                                                                                                                                                                                               9495,
                                         lethal with altered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Map position: 1
;Introns: 33/1; 63/3; 96/3
:sumerfamily: yeast nuclear transport factor NTF2
                                                                                                                                                                                                                                                                         bmitted to the EMBL Data Library,
Reference number: Z19818
Accession: T23921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: yeast nuclear transport factor NTF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-84 <HAW>
                                                                                                                                                                                                          Residues: 1-133 <WIL>
                                                                                                                                                                                                                             Molecule type: DNA
                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                            Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             pothetical protein R05D11.3 - Caenorhabditis elegans
                                                                                                                                                            Cross-references: EMBL:275546; PIDN:CAA99890.1; GSPDB:GN00019; CESP:R05D11.3 Experimental source: clone R05D11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: SGD:S0000811; MIPS:YER009w
iap position: 5R
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                                                                                                                                                                                                                                                                                                                                                                           Accession:
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                                                                                                             CESP: R05D11.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 TCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCAAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 GACACATTGCCTTCTAGTGAGTTCCAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 ATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 IleAspGluGluGlnAsnProGlnArg -- . PheSerGlnValPheHisLeu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 ValSerLeuProPheGlnLysValGlnHisArgIleThrThrLeuAspAlaGlnProAla 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 SerProAsnGly--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCACTCCCAACAATACTGTGTGGAAGATTGCAAGTGATTGCTTCCGT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---IleProAspGlyAsnSerTyrTyrValPheAsnAspIlePheArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGAT-----GGAAACAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerMetLeuThrPheGluThrSerGlnLeuGlnGlyAlaLysAspIleValGluLysLeu 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLeuAspPheAsnThr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corbett, A.; Kweon, Y.; Petzold, A.S.; Silver, P.; Brown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.91%
27.94%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GTCAATATGTTAGATTGCCAACCAGTT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LeuAlaGlnAsnPheThrGln 14
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38
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58
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Designation 19 26 77%
t Local Similarity: 26.77% Mismatches: 4
Local Similarity: 26.77% Mismatches: 4
Match: 4 04% Indels: 4
Match: 4.94% Indels: 1
2 Gaps: 6
2 Gaps:
*
-09-763-902B-15 (1-1146) x T23921 (1-133
206 GCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGA 25
11 AlaLysAlaPheIleGlnHisTyrTyrSerLysPheAspValGlyAspGlyMetSerArg
** ***********************************
251 AGACGGGACTATACCTTATCTGGACAGGCCACCTTAATATGGAATGGA
231 WANGARACIANCCARACIANICIARACANARCACCACCIINATATATATATATATATATATATATATATATATATATA
31 AlaGlnGlyLeuSerAspLeuTyrAspProGluAsnSerTyrMetThrPheGluGlyGln 5
100 0000000000000000000000000000000000
308 GCTGTTTCAGGGCTGGATGCCCTAAATATTTTTTTGACACATTGCCTTCTAGTGAGTTC
51 GlnAlaLysGlyArqAspGlyIleLeuGlnLysPheThrThrLeuGlyPheThrLysIle 7
368 CAGGTCAATATGTTAGATTGCCAACCAGTTCATGAGCAAGCAA
71 GloardalallomhrvallloasosorGlobrolloidvasogGlysorTloGlo 8
1. PINTALL TERROR TO THE STATE OF THE STATE
422 ACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAACAACAACAACTTTC 4
89ValMetValLeuGlvGlnLeuLvsThrAspGluAspProIleAsnPro 10
on the state of th
482 TTCAACCAGAACTTCCTGCTGACTGCTCAGTCCCAACAATACTGTGTGGAAG
105 PheSerGinValPheIleLeuArgProAsnAsnGlnGlvSerTvrPhe
539 ATTIGCAAGTGATTGCTTCCGT 55
· ====================================
121 IleGlvAsnGluIlePheArq
191 11001]:00010110:001
SUL
23479
voothetical protein KO8F4 2 - Caenorhabditis elegan
;species: caenornabultis eregans
:Date: 15-Oct-1999

7.1.10
to the EMBI, Data Library, January 19
to the minn para protary, ounderly to
;Reference number: 219746
Accession: T23479
DOCCOUNTED THE STATE OF THE STA
;Status: preliminary; translated from GB/EMBL/DDB
Molecule type: DNA
. Docidios . 1 537 VI
Residues: 1-33/ <will></will>
;Cross-references: EMBL:268879; PIDN:CAA93082.1; GSPDB:GN00022; CESP:K08F4.
- Strong + Cl. (Strong + Cl.
Experimental source: clone Kudr
Genetics:
CONC. CECT. VOCEA
Gene: CESP: KUSF4
:Map position: 4
TOTAL POST AND THE PROPERTY OF
trons: 66/3; 99/1; 140/3; 161/3; 338/1; 41
CTOHS: 00/0/ 00/1: TAO/0: TOT/0: 000/1: 41
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ent scores:
No.: 0.185 Length: 5
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94.00 Matches: 3
t cimilarity. A6 889 Conservative: 2
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though officially 80.000 historica.
ry Match: 4.67% Indels: 2
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-09-763-902B-15 (1-1146) x T23479 (1-53
-03-103-3040-13 (T-11-10) X (1906-13 (T-30
203 GCTGCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGA 25
203 GCTGCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGA 20
OF PARTICULAR OF THE PROPERTY
96 AlaKiaGinvarGiyGiyAlaPheCySHiSGinPheTyTileThiValSeTGIASh J

TATGGAATGGAAAT	Oy 146 AGGTCCCAGATGGCCACGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGA 202 :: :::::::::::::::::::::::::	Alignment Scores: Pred. No.: 94.00 Score: 94.00 Matches: 60 Percent Similarity: 40.75% Mismatches: 101 Query Match: 22.64% Mismatches: 101 Query Match: 23.64% Mismatches: 101 Query Match: 24.67% Gaps: 14 US-09-763-902B-15 (1-1146) x T04439 (1-1052) Qy 26 GGAAAATTTTGGCGTTTGGCGGGTTTCGTTCATAGTATTGATCATTCCGCAGC 85 :::	RESULT 9 T04439 T04439 hypothetical protein T18B16.150 - Arabidopsis thaliana C;Species; Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C;Accession: T04439 R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, H.W. submitted to the Protein Sequence Database, April 1998 A;Reference number: Z15359 A;Accession: T04439 A;Molecule type: DNA A;Residoues: 1-1052 <bev> A;Cross-references: EMBL:AL021687 A;Experimental source: cultivar Columbia; BAC clone T18B16 C;Genetics: A;Map position: 4 A;Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3 A;Note: T18B16.150</bev>	Oy AGACGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGCAATGCT 310
09-763-902B-15 (1-1146) x F86270.(1- 215 TTTGTCAATATTTACTATGAGACAA	Alignment Scores: 0.426 Length: 428 Score: 90.50 Matches: 30 Percent Similarity: 45.458 Conservative: 25 Best Local Similarity: 24.798 Mismatches: 53 Ouery Match: 4.508 Indeads: 13 DB: 4 Gaps: 4	Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Den Hughes, B.; Huizar, L. 2000 816-820, 2000 Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Rooney, T.; Rowley, D.; Sakano, H. Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; 'Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; 'D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. quence and analysis of chromosome 1 of the plant Arabidopsis. number: A86141; MUID:21016719; PMID:11130712 reliminary type: DNA 1-428 <sto> 1-428 <sto> erences: GB:AB005172; NID:g8920577; PIDN:AAF81299.1; GSPDB:GN00141</sto></sto>	Qy 644 TATTTTGATTGTAGAAGCACTATAATATGTGCTGAAACTAAATTTCTTTAATATTTTCTA 703 1021 PhePhe	Qy 308GCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTGACACATTGCCTTCTAGTGAG 364

Rt69B.1.

er glycoprotein; spike glycoprote ous peritonitis virus	· 	
precursor - feline infectious peritonitis virus		Qy 302 GGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTTT
Qy 586 GGGCAAAAGTCCATTCT 607		Oy 242 GATAAAAGAAGACGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAAT 301
Qy 526 TACTGTGTGGAAGATTGCAAGTGATTGCGTTTTCAAGATTGGTCTAGTAGTTAAAG ;;		QY 185 GTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCAATATTTACTATGAGACAATG 241 :::
Qy 482CCCAACAA	-	Qy 137 ACTGCTACAAGGTCCCAGATGGCCACGTCTCTGGATTTTAAAACTTAT 184
Db 775 lTyrThrSerSerThrGlnGlnTyrAspThrLeuProGlnAspIleMetIleLysGlnA147		-09-763-902B-15 (1-1146) x S24382 (1-643)
376 769		Score: 87.00 Matches: 40 Percent Similarity: 41.61% Conservative: 17 Best Local Similarity: 29.20% Mismatches: 62 Ouery Match: 4.32% Indels: 18 DB: 18
OY 316 AGGGCTGGATGCCCTAAATAATTTTTTTGACACTACTTCTAGTGAGTTCCAGGTCAA ::::::	<u>.</u>	ent Scores: 1.1 Length:
730		AA46383.1; PID:g387
Alignment Scores: Pred. No.: 86.00 Score: Percent Similarity: Best Local Similarity: Query Match: 2 Length: 86.00 Matches: 32 Conservative: 17 Mismatches: 50 Query Match: 2 Gaps: 4 Canservative: 17 Gaps: 4 Canservative: 17 Gaps: 4 Canservative: 17 Gaps: Canservative: 17 Gaps: Canservative: 17 Gaps: Canservative: 17 Gaps: Canservative: 18 Conservative: 19 Conservative: 19 Conservative: 17 Gaps: Canservative: 17 Gaps: Canservative: Canservative: Conservative: Conservative:	r, B. ctase) frc	C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999 .C;Accession: \$24382 R;Aumft; W.G.; Dreusch, A.; Loechelt, S.; Cuypers, H.; Friedrich, B.; Schneider, R;Zumft; W.G.; Dreusch, A.; Loechelt, S.; Cuypers, H.; Friedrich, B.; Schneider, Eur. J. Biochem. 208, 31-40, 1992 A;Title: Derived amino acid sequences of the nos2 gene (respiratory N(2)O reductaes. Implications for the Cu(A) site of N(2)O reductase and cytochrome-c oxidase. A;Accession: \$24382; MUID:92380183; PMID:1324835 A;Accession: \$24382
A;Gene: xynB C;Keywords: glycosidase; hydrolase		⊷ co
A;Molecule type: DNA A;Residues: 1-1595 <mor> A;Cross-references: EMBL:AF036923; NID:g2760904; PID:g2760908; PIDN:AAB95325.1</mor>		Db 131 Tyr 131 RESULT 11
to the EMBL Data Library, December 1997 tion: Family 10 and 11 xylanase genes from Caldicelluce number: 220972 on: T31082 preliminary; translated from GB/EMBL/DDBJ		Oy 500 CTGACTGCTCAGTCCACCAACAATACTGTGGGAAGATTGCAAGTGATTGCTTCCGT 559
ies: Caldicellulosituptor sp. 102-Sep-2000 #sequence_revision 02-Sep-2000 #ssion: T31082		QY 440 ACCAGTGGAACTGTGAAGTTTGATGGAAACAAACAATCTTCTTCAACCAGAACTTCCTG 499
RESULT 12 T31082 endo-1.4-beta-xvlanase (EC 3.2.1.8) - Caldicellulosiruptor sp		. 76
Qy 476 CATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCAGCAACAAT::526		
Qy 416 TCCCAAACTACAGTTCTTGTTGTGACCAGTGGAAGCTGTGAAGTTTGATGGAAACAAAC	=	
Db 435 LysTyrValValAspArgLeuAspLeuGlnTyrGlnProGlyHisValAsnAlaSerGln		GluLysTyrTyrAsnLeuLeuTyrLysSerProSerGlnVali AGGCCACCTTAATATGGAATGGAAAT

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R;De Groot, R.J.; Maduro, J.; Lenstra, J.A.; Horzinek, M.C.;
J. Gen. VIrol. 68, 2639-2646, 1987
A;Title: cDNA cloning and sequence analysis of the gene encoda, Reference number: A27171; MUID:88034948; PMID:3312491
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;1-19/Domain: transmembrane #status predicted <TMI>
;1-19/Domain: transmembrane #status predicted <TMI>
;20-1452/Product: spike glycoprotein #status predicted <SPG>
;1394-1414/Domain: transmembrane #status predicted <TM2>
;29,95,174,208,234,241,288,337,348,365,408,452,483,519,535;557,565,707,728,783,822,837
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GluIleProPheGlyIleThrAspGlyProArgTyrCysTyrValLeuTyrAsnGlyThr 410
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                                      TCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTA--
                                                                           SerCysTyrSerAspThrValSerGluSerSerSer-
                                                                                                                                                       SerGlyMetGlyAlaThrValPheSerLeuAsnThrThrGlyGlyValIleLeuGluIle
                                                                                                                                                                                                                                     SerLeuAsnAsnThrValAspValIleArgPheAsnLeuAsnPheThrAlaAspValGln
                                                                                                                                                                                                                                                                            TCATTTGGTCCATTAGTTCCAGCAATTGAAATTTATGTGAATTAT--
                                                                                                                                                                                                                                                                                                                                                        -----GATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAGGGGGCAAAAGTCCATTC
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A;Title: Subunit structure of the mammallan exocyst complex. A;Reference number: Z16617; MUID:98070770; PMID:9405631
A;Accession: T09221
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A; Residues: 1-822 <KEE>
A; Cross-references: EMBL: AF032668;
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LeuHisValThrGlnGlyLeuValThrArgAlaTyrThrAspGlu--
                                                                                                                                                     GlnArgLysLysGlnAlaArgLeuValLeuGlnProGlnSerSerValHisGluThrVal
                                                                                                                                                                                                                                   CysSerHisIleTyrSerAlaLeuGlyAspGluGluThrPheGluAsnTyrTyrArgLys
                                                                                                                                                                                                                                                                          ---ACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCAATATTTAC----
                                                                                                                                                                                                                                                                                                                   GluAsnAspGluGluValLeuThrValGlnAspLeuValAspPheSerProValTyrArg
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                                                                         AspGlyTyrArgArgTyrPheThrGlnIleValGlyPhePheValValGluAspHisIle
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	;Gene: F23010.17	
41	;Cross-references: GB:AEUU5173; NID:g77U5U97; PIDN:AAF67776.1; GSPDB:GN0014;Genetics:	900
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	sion: E96716 ogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul. S.	20 CO
	ble RNA-binding protein F23010.17 [imported] - Arab cles: Arabidopsis thaliana (mouse-ear cress) e: 02-Mar-2001 #sequence revision no-Mar-2001 #fort	0.00
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                         584 AGGGGCAAAAGTCCATTCTCATTTGGTCCATTAGTTCCAGCAATTGAAATT 634
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Search completed: June 24, 2003, 19:39:23 Job time: 48.4874 secs

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-OB-PUblished_Applications_AA -QFMT-fastan -SUFFIX-n2p_rapb -MINMATCH=0.1
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-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0
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Sequence 107, App
Sequence 272, App
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NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1180
LENGTH: 162
TYPE: PRI
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Best Local Similarity:
Query Match:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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Sequence 18, Appl
Sequence 119, Appl
Sequence 141, Appl
Sequence 141, Appl
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Sequence 315, Appl
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                                                                                                         Percent Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
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ITLE OF INVENTION: Nucleic Acids,
ILE REFERENCE: PTZ23
                                                                                            Local Similarity:
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PRIOR FILING DATE: 2000-(
NUMBER OF SEQ ID NOS: 184
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JS-09-791-932-107
                                                                                                                                                                                                                                                    Sequence 272, Application US/10074475 Publication No. US20030092898A1
                                                   APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating
TITLE OF INVENTION: Genes and Proteins
            CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
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Cafferkey, Robert
Sun, Yongming
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Best Local Similarity:
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                                                                                                                                                                                                 STATE: PA
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; PRIOR FILING DATE: 2001-02-13; NUMBER OF SEQ ID NOS: 295; SOFTWARE: PatentIn version 3.1; SEQ ID NO 272; LENGTH: 449; TYPE: PRT; ORGANISM: Homo sapien
US-10-074-475-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-763-902B-15 (1-1146) x US-10-074-475-272 (1-449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09854799 Patent No. US20020115064A1 GENERAL INFORMATION:
                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                     ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SmithKline Beecham, Corporation TITLE OF INVENTION: Recombinant Feline Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 TTCCGTTTTCAAGAT 568
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                    APPLICATION NUMBER: US/09/854,799 FILING DATE: 14-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheArgTyrGluAsp
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                            COUNTRY: USA
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Matches:
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                                                                                                    Version #1.25
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REFERENCE/DOCKET NUMBER: SBC 14532B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
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LENGTH: 1454 amino acids
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GluIleProPheGlyIleThrAspGlyProArgTyrCysTyrValLeuTyrAsnGlyThr 412
                                                                                                       GATTGTAGAAGCACTATAATATGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTG 709
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                                      TCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTA----
                                                                        SerCysTyrSerAspThrValSerGluSerSerSer
                                                                                                                                          SerGlyMetGlyAlaThrValPheSerLeuAsnThrThrGlyGlyValIleLeuGluIle
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Conservative:
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              Percent Similarity:
Best Local Similarity:
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US-09-854-799-24
   Query Match:
                                                       Score:
                                                                                       Alignment Scores:
                                                                                                                        MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: US-09-854-799-24
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/854,799
FILING DATE: 14-May-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Recombinant Feline Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SmithKline Beecham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430
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                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 LENGTH: 748 amino acids
                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                          NAME: King, William
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990
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                                                                                                                                            NO:
                Length:
Matches:
Conservative:
Mismatches:
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                RESULT 7
US-09-815-242-5373
Sequence 5373, Application US/09815242
Patent No. US20020061569A1
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US-09-815-242-5373
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-763-902B-15 (1-1146) x US-09-815-242-5373 (1-1127)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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LENGTH: 1127
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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
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                                                            476 CATTTC 481
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                232 GlnPhe 233
                                                                                                       GlyLeuIleLysTyrAlaLysSerValThrIleIleLeuThrThrAspGlyAsnHisAsp 231
                                                                                                                                                   GGAACTGTGAAGTTT - -
                                                                                                                                                                                                                                            CAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTT----CTTGTTGTGACCAGT
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Yamamoto, Robert T.
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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IS-09-815-242-12522
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ENGTH: 1158
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APPLICATION NUMBER: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                 162 LeuIleTyrArgGluPheGluGlnArgIleGlnAsnGluPheIleThrGlyGluAspAla
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                                                                                                            389 CAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTT---CTTGTTGTGACCAGT
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GlyLeuIleLysTyrAlaLysSerValThrIleIleLeuThrThrAspGlyAsnHisAsp 237
                                                                                                                                                 LeuGlnTyrPheIleAspCysMetProLysSerGluTrp--
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Zyskind, Judith W.
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; ORGANISM: Homo sapiens
US-10-176-847-52
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 752
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GENERAL INFORMATION
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US-10-077-130-5
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SOFTWARE: FastSEQ for
SEQ ID NO 5
LENGTH: 7968
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PRIOR FILING DATE: 2001-02-15
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                                                                                                                                                                                                                                                            TYPE: PRT
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PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
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                                                                                                                                                    ORGANISM: Homo sapiens
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FILING DATE: 1998-12-18
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                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/043,476
PRIOR FILING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: PCT/IB96/0113
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB9612368.2
PRIOR FILING DATE: 1996-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/139,876
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                     LENGTH: 358
TYPE: PRT
ORGANISM: Mus musculus
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rILE REFERENCE: 35784/205172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09854799 Patent No. US20020115064A1 GENERAL INFORMATION:
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,459
FILING DATE: <UNknown>
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  CURRENT
                                                                                                                                                                                                                                                                                                                                                          COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SmithKline Beecham, Corporation TITLE OF INVENTION: Recombinant Feline Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
RENT APPLICATION DATA:
APPLICATION UMBER: US/09/854,799
FILING DATE: 14-May-2001
CLASSIFICATION: CUnknown>
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                       NAME: King, William T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                          TER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Smithkline
STREET: 709 Swedeland
CITY: King of Prussia
    REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                            353 AlaAspValGlnSerGlyMetGlyAlaThrValPheSerLeuAsnThrThrGlyGlyVal 372
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  AsnGlyThrAlaLeuLysTyrLeuGlyThrLeuPro
                                                                                                                       CTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCCTCTA-----
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                                                                             SerTyrGlyGluIleProPheGlyIleThrAspGlyProArgTyrCysTyrValLeuTyr
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                                         --AGAGCTTTAAAAACTATTTTTTACATGCCTTATATACATTCCACTAATGACATT 808
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215) 270-5090
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Conservative:
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-ProSerValLysGluIle
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QY 290 TTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTTGACACA 349	Qy 248 AGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCACC 289	Qy 209 GAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAA 247 ::::::::::::::::::::::::::::::::::::	US-09-763-902B-15 (1-1146) x US-10-156-239-11 (1-450)	Alignment Scores: 2.73 Length: 450 Pred. No.: 78.50 Matches: 31 Score: 78.50 Matches: 31 Percent Similarity: 43.27% Conservative: 14 Best Local Similarity: 29.81% Mismatches: 30 Ouery Match: 3.90% Indels: 29 DB: 6	; SEQ ID NO 11 ; LENGTH: 450 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-156-239-11	Z Z	FILING DATE: 2001-03-14 APPLICATION NUMBER: 60 FILING DATE: 2000-03-24	APPLICATION N APPLICATION N	PRIOR APPLICATION NUMBER: 60/185,906 PRIOR FILING DATE: 2000-02-29 PRIOR APPLICATION NUMBER: 09/809,557 PRIOR FILING DATE: 2001-03-15	NT APPLICATION NUMBER NT FILING DATE: 2003 APPLICATION NUMBER: FILING DATE: 2001-0	NT: Kapeller-Libermann, Faller R. NT: Kapeller-Libermann, Finvention: No. US20030 FINVENTION: ATPase Moler INVENTION: Ubiquitin FERENCE: 35800/247645	-11 , Application No. US200300 ORMATION:	Db 475 euValGlnValGluAsnThr 481		Db 437 IleAsnGlyTyrAsnPhePheSerThrPheProIleAspCysIleSerPheAsnLeuT 456 Ov 926 CTCTGGGAAGAAGTGGAGTTTTTTGGTTTAGTTTAGTTT	. 869	GTGAACCCAGCCTA
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NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT
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IST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=1
DDE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500
                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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/Cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/Cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/Cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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                                             FILING DATE: 13-MAY-PRIOR APPLICATION NUMBER:
                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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NAME:
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	equence 2	equence 42, Ap	equence 42, Ap	equence 28, Ap	equence 37	equence 12	equence 5,	Sequence 3, Appl	equence 42	equence 25	equence 4;	equence 2,	equence 10	equence 6,	ence 6,	equence 6,	equence 6,	uence 16	equence 8,	uence 26	equence 26	equence 6,	equence 34	equence 28	equencë 34	equence 28	equence 9,	quence 48	equence 12	equence 32	equence 32	quence 9,	equence 46	

ALIGNMENTS

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           SOFTWARE: Patentin Rei
                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 13-MAY-1991
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                DOCKET NUMBER
                                                                                                                                                                                                                                          PatentIn Release #1.0,
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9 Swedeland
                              William T
                                                                           NUMBER: US 07/613,066
14-NOV-1990
INFORMATION
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US-09-763-902B-15 (1-1146) x US-08-392-459-22 (1-1454)
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TELEFAX: (215) 270-5090
[INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                AlaLeuLysTyrLeuGlyThrLeuPro-----ProSerValLysGluIleAlaIle---
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GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corn
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SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08525
FILING DATE: 19911114
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 13-MAY-1991
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TyrGlnGlyValSerAsnPhe
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Recombinant Feline Coronavirus
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GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
                                                                                            TITLE OF INVENTION: Compositions and Methods TITLE OF INVENTION: Against Coronaviruses NUMBER OF SEQUENCES: 48
                                                                            CORRESPONDENCE
                                                                                                                                                          APPLICANT:
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Reed, Albert Paul
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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No.
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 13-MAY-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/613,066	APPLICATION NUMBER: US 07/882,171 FILING DATE: 08-MAY-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/698,927	APPLICATION NUMBER: PCT/US93/04384 FILING DATE: 19930507 CLASSIFICATION: PRIOR APPLICATION DATA:	Patentin R	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPAtible OPERATING SYSTEM: DC-1005 MG-1005	BE 27	ADDRESSEE: Patents STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA	ୁଅନ	Klepfer, S Reed, Albe Jones, Ela NVENTION: C	H B	 alGluAsnThr		TAAAAICTTTTAIAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGATGTCAGCACACATATAACACTCTGGGATGTCAGCACATATAACACTCTGGGATGTCAGCACATATAAC		GCTTTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATA	710 TCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGA 757	650 GATTGTAGAAGCACTATAATATGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTG 709 	647TTT 649 357 SerGlyMetGlyAlaThrValPheSerLeuAsnThrThrGlyGlyValIleLeuGluIle 376	/ 602 TCATTTGGTCCATTAGTTCCAGCAATTGAAATTTATGTGAATTAT	
Qy 758 GCTTTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATA 817	Qy 710 TCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGA 757 Db 393 GluileProPheGlyIleThrAspGlyProArgTyrCysTyrValLeuTyrAsnGlyThr 412	Qy 650 GATTGTAGAAGCACTATAATATGTGCTGAAACTAAAATTTCTTTAATATTTTCTATTCCTG 709	7	7	Qy 602 TCATTIGGTCCATTAGTTCCAGCAATTGAAATTTATGTGAAATTAT 646	Qy 548GATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAGGGGCAAAAGTCCATTC 601	Db 301 ThrAsnGlnProLeuLeuIleAsnCysLeuTrpProValProSerPheGlyValAlaAla 320	Qy 479 TTCTTCAACCAGAACTTCCTGCTGATCGATCCACT	Qy 419 CAAACTACAGTTCTTGTTGTGACGAGACTGTGAAGTTTGATGGAAACAAAC	Qy 380 TTAGAT	Qy 320 CTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATG 3.79 :::::: Db 231 TyrGlnGlyValSerAsnPheThrTyrTyrLysLeuAsnAsn 244	Qy 260 CTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAAATGCTGTTTCAGGG 319 ::: :::	4.32% Indels: 5 Gaps: -15 (1-1146) x PCT-US93-04384-47 (1-1454	NO: Simila	MOLECULE TYPE: protein PCT-US93-04384-47 Alignment Scores	FOR SEQ. ID NO: 47: CHARACTERISTICS: 1454 amino acids AMINO ACID	TELEPHONE: (215) 270-5090 TELEPAX: (215) 270-5090	DATE: 14-NOV-1990 AGENT INFORMATION: Schreck, Pattica A. ATION NUMBER: 33,777	

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE:
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,685
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TYPE: amino acid
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CLASSIFICATION: 435
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    Application US/08591685
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TACTGTGGGAAGATTGCAAGTGATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAG
                                   aLeuLysPheLysGluLeuPheGluMetLeuLysArgHisSerAspArgIleThrAsnVa 366
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US-09-763-902B-15 (1-1146) x PCT-US93-04384-44 (1-1454)
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Best Local Similarity:
Query Match:
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PCT-US93-04384-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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TITLE OF INVENTION: Against Coronaviruses
NUMBER OF SEQUENCES: 48
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REFERENCE/DOCKET NUMBER: SBC H85009-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 08-MAY-1992
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ADDRESSEE: Patents
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211 ValThrLeuLeuTyrSerArgSerSerThrAlaThrTrpGluTyrSerAlaAlaTyrAla 230
                   382 gSerAsnTrpProLeuLeuPhe 389
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ADDRESSE: Pacental STREET: 709 SedeCaland Road CITY: King of Prussia STREET: 709 SedeCaland CONTRE: PA COUNTRY: USA COUNTRY: PC-005/M5-Dos COUNTRY: PC-005/M5-Dos COUNTRY: COUNTRY COUNTRY: USA COUNTRY:	undesse: surthythe beendu colbotation - colbotate	ron Paul e V. positions and Methods f inst Coronaviruses	45 Application PC/TUS	1 479 luAsnThr 481	-GTGGAGTT	AATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAAGAA	414 LeuLysTyrLeuGlyThrLeuProProSerVallysGluIleAlaIle 429 821 TTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAAAAATAA 880 :::	TTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATAATA	GCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGAGCT	668 ATATGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTGTCA 712	647ATA 667	602 TCATTTGGTCCATTAGTTCCAGCAATTGAAATTTATGTGAATTAT	548GATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAGGGGCAAAAGTCCATTC 601 	518 CCCAAC AATACTGTGTGGAAGATTGCAAGT 547	479 TTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACT	419 CAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAACAAAC	380 TTAGATTGCCAACCAGTTCATGAGCAAGCAAGTCAGTCC 418 ::: ::: :::	320 CTGGATGCCCTAAATAATTTTTTTGACACACATTGCCTTCTAGTGAGTTCCAGGTCAATATG 379 231 TyrGlnGlyValSerAsnPheThrTyrTyrLysLeuAsnAsn 244
ADDRESSE CITY: K: STREET: CITY: K: STATE: I COUNTRY: ZIP: COUNTRY: COMPUTER RI MEDIUM T: COMPUTER RI MEDIUM T: CORPUTER RI MEDIUM T: CORPUTER OPERITING DI CLASSIFI PRIOR APPLICAT: FILING DI CLASSIFI PRIOR APPLICAT: APPLICAT: APPLICAT: APPLICAT: APPLICAT: APPLICAT: FILING DI PRIOR APPLICAT: APPLICAT: TELEPHON. NAME: S: REFERENCY: TELEPHON. TELEPHON: TELEPHON: TELEPHOLOGY MOLECULE T: TYPE: APPLICAT: TYPE: NO:: COR: SEQUENCE C: LOCAL SIMILAR TOPOLOGY MOLECULE: APPLICAT: TOPOLOGY MOLECULE: APPLICAT: TOPOLOGY	• -			······································	<u> </u>	•	•			• 		<u></u> , <u>-</u>					.	
3		479 T 281 S 518 C 301 T	419 C 264 A	380 TTAGAT	320 CTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTC	260 C	Local Similarity: 35.20% Conservative: Local Similarity: 23.68% Mismatches: Watch: 4.27% Indels: Gaps: 5.763.0038-15 (1.1146) % pcm.rco3.04384-45 (1.146)	nment Scores: 0.0784 Length: .No.: 86.00 Matches:	POLOGY: unk CULE TYPE: 04384-45	CHARACTERISTICS: 1454 amino aci AMINO ACID	NICATION INFORMATION: NE: (215) 270-5015 : (215) 270-5090	AGENT INFORMATION: Schreck, Patrica A. SCHRECK 33,777 RATION NUMBER: 33,777	ATE: 13-MAY-199 ICATION DATA: ION NUMBER: US	ION NUMBER: US ATE: 08-MAY-199 ICATION DATA:	ION NUMBER: 1993050 CATION:	: IBM PC compatible G SYSTEM: PC-DOS/MS-DOS : Patentin Release #1.0, Version #1.	: USA 9406-27 READABI	SEE: Patents : 709 Swedeland King of Prussia

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RESULT 8
US-08-392-459-24
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
UMBER OF SEQUENCES:
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                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                              FILING DATE:
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ZIP: 19406-2799
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INFORMATION FOR SEQ ID NO:
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             ATATTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCCAGCCTATTGCAAAAA 877
                                                                                                                      GluIleProPheGlyIleThrAspGlyProArgTyrCysTyrValLeuTyrAsnGlyThr
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                                                 AlaLeuLysTyrLeuGlyThrLeuPro----ProSerValLysGluIleAlaIle---
                                                                                   GCTTTAAAACTATTTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATA
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US-09-763-902B-15 (1-1146) x PCT-US91-08525-24 (1-748) Qy 260 CTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGG 319 :::	Pred. No.: 0.0749 Length: 748 Score: 85.00 Matches: 69 Percent Similarity: 33.77% Conservative: 34 Best Local Similarity: 22.62% Mismatches: 112 Ouery Match: 4.22% Indels: 90 DB: 5 Gaps: 17	AMINO ACII Y: linea TYPE: pro -24	TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 270-5015 TELEFAX: (215) 270-5090 INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: IERUSTH. 748 smid-seide	ATTORNEY/AGENT INFORMATION: NAME: King, William T. REGISTRATION NUMBER: 30,954 REFERENCE/DOCKET NUMBER: SBC 14532B	APPLICATION NUMBER: US 07/698,927 FILING DATE: 13-MAY-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990	CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91/08525 FILING DATE: 19911114 CLASSIFICATION: 435 PRIOR APPLICATION: 435	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	russia	SEQUE ENCE	8525-24 24, Application PC/TUS9108525 INFORMATION: CANT: SmithKline Beecham, Corporation	Qy 995 TTAACACT 1002 Db 478 alGluAsnThr 481	Qy 935 GAAGTGGAGTTTTTTGGTTAATTAGGTTAATATTTCTAGTAAAACACGTTGCCTGTTTTCAG.994	Db 430SerLysTrpGlyHispheTyrIleAsnGly 439 Qy 878 TAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAACACTCTGGGAA 934
OF INV OF SE PONDEN	RESULT 10 PCT-US93-04384-4 ; Sequence 4, Application PC/TUS9304384 ; GENERAL INFORMATION: ; APPLICANT: Miller, Timothy J. ; APPLICANT: Klepfer, Sharon ; APPLICANT: Reed albert Paul	Db 459 alSerGlyAlaPheTrpThrIleAlaTyrThrSerTyrThrGluAlaLeuValGlnV 478 Oy 995 TTAACACT 1002	TTTTATAATATTATCTATGGGATGTCAGCACAI 	Qy 818 ATATTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAAAAA 877	Qy 758 GCTTTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATA 817	377 SerCysTyrSerAspThrValSerGluSerSerSerTyrSerTyrGly 710 TCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTAAGA	Db 357 SerGlyMetGlyAlaThrValPheSerLeuAsnThrThrGlyGlyValIleLeuGluIle 376 Qy 650 GATTGTAGAAGCACTATAATATTGTGCTGAAACTAAATTTCTTTAATATTTTCTATTCCTG 709	Qy 602 TCATTTGGTCCATTAGTTCCAGCAATTGATATTATGTGAATTAT	Qy 548GATTGCTTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAGGGGCAAAAGTCCATTC 601	AsnTrpheLeuLeuThrAsnSerAATACTGTGTGG ::: ProLeuLeuIleAsnCysLeuTrp	Qy 479 TTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCAGT	Db 245 ThrAsnGlyLeuLysThrTyrGluLeuCysGluAspTyrGluHisCysThrGlyTyr 263 Qy 419 CAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGAAACAAAC	Qy 320 CTGGATGCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATG 379 Comparison of the compariso

231 TyrGlnGlyValSerAsnPheThrTyrTyrLysLeuAsnAsn 244 Qy 380 TTAGATTGCCAACCAGTTCATGAGCAAGCAAGTCAGTCC 418 Qy 380 TTAGAT	Ignment Scornad No.: Te: Te: Tcent Simila Tcent Simila Tcent Sim Tocal Sim Tcent Sim T	ATTORNEY AGENT INFORMATION: NAME: Schreck, Patrica A. REGISTRATION NUMBER: 33,777 REGISTRATION NUMBER: 35C H85009-1 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 270-5015 TELEPAX: (215) 270-5015 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 748 amino acids TYPE: AMINO ACID TOPOLOGY: 11near MOLECULE TYPE: protein PCT-US93-04384-4.	APION NU ADATE: FICATION PPLICATION DATION DATION DATE: PPLICATION DATION DATION CATION CATION DATE: CATION CATION CATION DATE: DAT	ADDRESSEE: Patents STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA COUNTRY: USA ZIP: 19406-2799 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC:DOS/MS-DOS SOTTWARE: Patentin Release #1.0, Version #1.25 CURRENT ApplicAtion DATA:
Washington DC United States of An 0005 READABLE FORM: TYPE: Floppy disk R: IBM PC compatible RC SYSTEM: PC-DOS/MS- E: PPLICATION DATA: TION NUMBER: US/08/91 TION NUMBER: US/08/91 TION NUMBER: 26,269 ATION NUMBER: 26,269 ATION NUMBER: 106,269 CE/DOCKET NUMBER: 106 NICATION INFORMATION: NICATION INFORMATION: 106	SULT 11 Sequence 8, Application Patent No. 6235713 GENERAL INFORMATION: APPLICANT: Marc G. J. APPLICANT: Steven APPLICANT: Steven APPLICANT: Karl ALI: TITLE OF INVENTION: NUMBER OF SEQUENCES; CORRESPONDENCE ADDRESSEE: Evensoi	Qy 818 ATATTAAACACATGATCTTĞGTACTAACATACTCACTGTAACCCAGCCTATTGCAAAAA 877	Qy 650 GATTGTAGAAGCACTATAATATTGTGCTGTAAAATTTCTTTAATATTTTCTATTCCTG, 709 1 1 1 1 1 1 1 2 377 SerCystyrSerAspthrValSerGluSerSerSer	Oy 548GATTGCTTCCGTTTTCAAGATTGGTCTAGTAGTTAAAGGGGCAAAAGTCCATTC Db 321 GlnGluPheCysPheGluGlyAlaGlnPheSerGlnCys

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                       quence 43, Application:
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ORIGINAL SOURCE:
TISSUE TYPE:
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LENGTH: 358 amino acids
TYPE: amino acid
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                                                                          ITLE OF INVENTION: Compositions and Meth
ITLE OF INVENTION: Against Coronaviruses
WHER OF SEQUENCES: 48
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                                                                                                                                                                                         Miller, Timothy J.
                                                                                                                                     ones, Elaine V
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Best Local Similarity:
Query Match:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 07/613,066
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                           CysThrGlyTyrAlaThrAsnValPheAlaProThrValGlyGlyTyrIleProAspGly
                                                                                                                                               GCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTGATGGA 466
                                                                                                                                                                                             GlyLeuLysThrTyrGluPhe---
                                                                          AACAAACAACATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACT--
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Sequence 46, Application PC/TUS9304384 GENERAL INFORMATION:
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Miller, Timothy J.
                                                    APPLICATION NUMBER: P
FILING DATE: 19930507
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APPLICATION NUMBER:
                                  CLASSIFICATION:
                                                  FILING DATE:
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LE OF INVENTION: Against Coronaviruses
BER OF SEQUENCES: 48
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                  APPLICATION DATA:
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King of Prussia
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Reed, Albert Paul
Jones, Elaine V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: (215) 270-5015
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REFERENCE/DOCKET NUMBER:
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Matches:
Conservative:
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INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 321 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: TISSUE TYPE: Mouse Lung S-08-915-795-9	COMPUTER: IBM PC FOR THE COMPUTER: IBM PC FOR THE COMPUTER: IBM PC FOR THE COMPUTER: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NOATA: APPLICATION NUMBER: US/08/915,795 FILING DATE: CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: EVANS, JOSEPH D. REGISTRATION NUMBER: 1064/42983 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-8844 TELEX: N/A TELEX: N/A		NFORM NT: NT: NT: NT: OF SE ONDEN	Qy 983 GCCTGTTTTCAGTTAACACT 1002	Qy 866 CTATTGCAAAAATAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAAC- 924 :::	Db 373 IleLeuGluIleSerCysTyrSerAspThrValSerGluSerSerSer 388 Oy 698 TTTCTATTCCTGTCAGCACCTTTTCTAGCAGCTTTGGAGCATTGGCCCTCTA 754 :::
ZIP: 19406-2799 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION: 435 PRIOR APPLICATION UMBER: US/08/392,459 PRIOR APPLICATION NUMBER: US 07/698,927	RESULT 15 US-08-392-459-32 Sequence 32, Application US/08392459 Patent No. 6280974 GENERAL INFORMATION: APPLICANT: SmithKline Beecham, Corporation TITLE OF INVENTION: Recombinant Feline Coronavirus S TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 54 CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA COUNTRY: USA	Qy 87 GGGCTGCGAATGATACTTATGAAGAGGGGAAACCCGCCAAACGCACAAAT 31	Qy 107	OY 222 TIGACAAACTCCTCAGCAGGTCTACATGCCTGATCTACATAAGTTTTAAAATCCAGAGAC 163 :::::::::::::::::::::::::::	QY 327 GCATCCAGCCCTGAAACAGCATTTCCATTCCATATTAAGGTGGCCTTGTCCAGATACAGC 268	Alignment Scores: Pred. No.: 80.00 Percent Similarity: 22.568 Best Local Similarity: 22.568 Conservative: Query Match: 3.958 DB: US-09-763-902B-15 (1-1146) x US-08-915-795-9 (1-321) Qy 387 CAATCTAACATATTGACCTGGAACTCACTAGAAGGCAATGTGTCAAAAAAATTATTAGG 328 DB: 148 GluGluGlyValMetCysMetAsnThrSerTyrIleSerLysGlnLeuPheGlu 167

APPLICATION NUMBER: US 07/613,066 FILING DATE: 14-NOV-1990

13-MAY-1991

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REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
LECOMMUNICATION INFORMATION:
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                                            --GCTGAAACTAAATTTCTTTAATATTTT 700
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		Db .
	986 TGTTTTCAGTTAACACT 1002	Qy
475	456 hrThrGlyAspSerGlyAlaPheTrpThrIleAlaTyrThrSerTyrThrGluAlaL 475	Db
985	926 CTCTGGGAAGAAGTGGAGTTTTTTGGTTATTAGGTTAATTTTCTAGTAAAACACGTTGCC 985	Qy
456	erThrPheProIleAspCysIleSe	рb
925	869 TTGCAAAAATAAAATCTTTTTATAATATTATCTATGGGATGTCAGCACAATATAACA 925	Qy
436	428 Alaile SerLysTrpGlyHisPheTyr 436	Db
868	809 CTTATAATAATAATAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTA 868	Qy
427	410 AsnGlyThrAlaLeuLysTyrLeuGlyThrLeuProProSerValLysGluIle 427	Db
808	755AGAGCTTTAAAACTATTTTTTACATGCCTTATATACATTCCACTAATGACATT 808	Qy
409	390 SerTyrGlyGluIleProPheGlyIleThrAspGlyProArgTyrCysTyrValLeuTyr 409	Db
754	701 CTATTCCTGTCAGCACCTTTTCTAGCAGCTGCCAGTTTGGAGCATTGCCCTCTA 754	Qy

Search completed: June 24, 2003, 19:40:32 Job time: 32.789 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Result ö

SUMMARIES

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Title:
Perfect score:
                                                                                                                                   Run on:
                                                                                                                                                                    OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                             June 24, 2003, 19:20:48; Search time 54.8062 Seconds
                          US-09-763-902B-15
2013
  tacttccgggagagaatggg...
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5572.555 Million cell updates/sec
...ttttaagtaatttttgtttt 1146
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Scoring table: Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 908470 seqs, 133250620 residues 7.0 7.0

Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: 1816940

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame+_n2p.model -DEV-xlp

LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR MODE-LOCAL -OUTEMT-pco -NORM-ext -HBAPSIZE-500 -MINLER USER-USO9763902_eGGN_1_162_ecunat_24062003_130340_12 NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLCCK-100 DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 DB-A_Geneseq_101002 -QFMT-fastan -SUFFIX-n2p.rag 0=/cgn2_1/USPT0_spoo1/US09763902/runat_24062003_130340_12405/app_query.fasta_1.2254 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 -1 -MATRIX-blosum62 -TRANS-human40.cd1 -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 12405 -NCPU-6 -ICPU-3 -MAXLEN-2000000000

Database : A_Geneseq_101002:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT AA1984 . DAT : .DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESU	LT 1	
AAB95379	5379	
ij	AAB95379 standard; Protein; 197 AA.	
X	:	
ÃC	AAB95379;	
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ij	26-JUN-2001 (first entry)	
XX		
DE	Human protein sequence SEQ ID NO:17707.	
×		
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy.	
×		
SO	Homo sapiens.	
X		
PN	EP1074617-A2.	
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PD	07-FEB-2001.	
XX		
PF	28-JUL-2000: 2000EP-0116126	

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DB:
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as a sily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the secification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
Ishii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent oligonucleotides, of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB95893 represent human amino acid sequences; and AAH13629 represent oligonucleotides, all of which are used in the exc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
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, Sugiyama
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                                              CGGGCACTAACCAGGCTGTATCTGGACAAGGCCACCTTAATATGGAATGGAAATGCTGTT
                                                                                         AlaCysArgAlaAlaGluGluPheValAsnIleTyrTyrGluThrMetAspLysArgArg
                                                                                                          HisThrAlaThrArgSerGlnMetAlaThrSerLeuAspPheLysThrTyrValAspGln
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T, Wakamatsu
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Matches:
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Otsuki
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     molecules (PTAMS) given in AAY82317 to AAY82324. The PTAMS have cytostatic, antiarthritic, antiasthmatic, immunosuppressant, antiarteriosclerotic, antiallergic, antidiabetic, antiipsemic, antirheumatic, osteopathic, dermatcological, antianaemic, antipsoriatic, hepatotropic, antiquout, antiinflammatory and antiHTV activities, and regulate protein transport. PTAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased expression or activity of PTAM. PTAM, polynucleotides are useful for diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; protein transport molecule; PTAM; diagnosis; antiarthritic; antiathmatic; immunosuppressant; ant antialleggic; antidiabetic; antilipeemic; antirheum dermatological; antianaemic; antipsoriatic; hepatot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY82323;
                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                      New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                           Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; antiHIV; protein transport regulator; cancer; immune disorder; cell proliferative disorder; secretory disorder;
                                                                                                                                                                                                                                                                                                                                                                       2000-256642/22
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                                                                                                                                                                                                                                Page 68;
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                                                                                                                                                                                          AAA08042 encode the human protein transport-associated
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                                                                                                  Human NTF2 associated protein
                                                                                                                              04-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           into cells or tissues expressing PTAM and for diagnosis of PTAM related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biological sample. Diseases prevented, treated or diagnosed incl
proliferative disorders such as cancers, immune disorders, secre
disorders and other conditions associated with abnormal vesicle
trafficking, such as allergies, asthma, urticaria and autoimmune
  19-SEP-2001
                                                                           Human; NTF2
                                                                                                                                                                               ABB04459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and NTF2 associated protein 16. The sequences can teamer and HIV infection, as well as other dise is the protein of the invention.
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07-NOV-2001

(first entry)

AAU16227;

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standard;

Protein;

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22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000
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04-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiaca arrest, cerebrovascular disorders e.g. cardiaca arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
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Rosen CA, Barash SC, Ruben SM

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Claim 11; SEQ ID No 1181; 980pp; English

The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses; cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoassays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. englasms of the breast or liver, cardiovascular disorders e.g. cardiae arrest, cerebrovascular disorders e.g. cardiae arrest, cerebrovascular disorders e.g. cardiae infection, and many other cardiovascular disorders e.g. corneal infection, and many other allowed to aid wound healing and epithelial cell proliferation, to prevent skin aging due to supphyrn. Fo maintain organs before capabilities, fat content, lipid, protein, carbohydrate, minerals, cofactors and other nutritional components. The sequence represents a novel secreted protein of the invested protein of the investe prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage The present vitamins used

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immune disorder; cell proliferative disorder; secretory disorder;
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dermatological; antianaemic; antipsoriatic; hepatotropic; antigout;
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antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic;
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haemolytic anaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human protein transport-associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis - :
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                                                                                                                                                                                                                           344 GACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATGAG
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                AATACTGTGTGGAAGATTGCAAGTGATTGCTTTCCGTTTTCAAGATTGGTCTAGT
                                                                                                                                            TCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCAAT
                                                                              GGAAACAAACATTTCTTCAACCAGAACTTCCTGCTGATGCTGCTCAGTCCACTCCCAAC
                                                                                                                                                                                                                                                                                                                           ValTyrTyrThrThrMetAspLysArgArgArgLeuLeuSerArgLeuTyrMetGlyThr
                                                              GlyAsnLysGlnArgAspPheAsnGlnAsnPheIleLeuThrAlaGlnAlaSerProSer
                                                                                                                            GluAlaThrProSerGlnThrThrValLeuValValIleCysGlySerValLysPheGlu
                                                                                                                                                                                           GluMetLeuProSerSerGluPheGlnIleSerValValAspCysGlnProValHisAsp
                                                                                                                                                                                                                                                           AlaThrLeuValTrpAsnGlyAsnAlaValSerGlyGlnGluSerLeuSerGluPhePhe
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
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N-PSDB; ABL09120.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence data for this patent did not form part of the printed ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                      290 TTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTTTTGACACA 349
                                                                                                             230 TATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACAAGGCCACC
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RESULT 8
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Sequence 688 AA;
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genes from Drosophila
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  Disclosure; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheAsnAspCysHisAlaLysIleSerGinValAspAlaGinAlaThrLeuGlyAsnGly
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          Arabidopsis thaliana
                                          Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter
                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 11042.
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                                                                                                                      AAG12073;
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                                 termination
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGHTG-ABLIGHT), expressed DNA sequences (ABLIGHTG-ABLIGHT), expressed DNA sequences (ABLIGHTG-ABLIGHT).
                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                              Length:
Matches:
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Gaps:

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                                                                                                     ThrGlnThrPheValLeuAlaAlaGlnSerProLysLys-
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Query Match:
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                                                                      71 ValAspSerGlnPro-----SerSerMetAlaGlyGlyCysGlyGlyIleLeuValPhe
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                                                                                                                                                                                                                       11 AlaSerAlaPheValAsnHisTyrTyrHisLeuPheAspAsnAspArgSerSerLeuSer
                                                                                                                                                                                                                                                       206 GCTGAGGAGTTTGTCAATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACC
CTGCTGACTGCTCAGTCCACTCCCAACAATACTGTGTGG 535
                                                 ACCAGTGGAACTGTGAAGTTTGATGGAAACAACAACATTTC---TTCAACCAGAACTTC
                                                                                      GCCCTAAATAATTTTTTTGACACATTGCCTTCTAGTGAGTTCCAG-----GTCAATATG
                                                                                                                                                                           SerLeuTyrAsnProThrSerLeuLeuThrPheGluGlyGlnThrIleTyrGlyValAsp
                          ValSerGlySerIleGlnLeuHisGlyGluAspHisProLeuArgPheSerGlnValTyr
                                                                                                                                                                                                    99US-0161992.
99US-0161993.
99US-0162142.
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AAG05145
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25-MAY-1999;
27-MAY-1999;
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             99US-0137528
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99US-0139419
99US-0139452
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US-09-763-902B-15 (1-1146) x AAG05145
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Percent Similarity:
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Query Match:
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158 GCCACGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTT
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9908-0149929

9908-0149929

9908-015066

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21
                                              (1-153)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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18-JUN-1999
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28-JUL-1999
02-AUG-1999
02-AUG-1999
03-AUG-1999
04-AUG-1999
04-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
06-AUG-1999
10-AUG-1999
11-AUG-1999

13 SerAlaSerLeuSerLeuLysMetSerGlnMetAspProAspAlaValSerLysAlaPhe

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9905 0144325 9905 0144331 9905 0144332 9905 0144335 9905 0144535 9905 0144508 9905 014508 9905 014508 9905 014508 9905 014508 9905 014508 9905 014514 9905 014524 9905 014524 9905 014521 9905 014521 9905 014521 9905 014538 9905 014538 9905 014538 9905 014538 9905 014538 9905 014538 9905 014538 9905 014538 9905 014730 9905 014731

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     99US-0132485.
99US-0132486.
99US-0132487.
99US-01324863.
99US-0134256.
99US-0134218.
99US-0134218.
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99US-0134271.
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S-0123548.
S-0125788.
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27-JUL-1999;
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                 99US-0145087
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99US-0145192
99US-0145145
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99US-0134941
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RESULT 13
AAG08681
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                      AAG08681;
                                                                          25-FEB-2000;
                                                                                                  06-SEP-2000
                                                                                                                         EP1033405-A2.
                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 6316.
                                                                                                                                                                                                                                               17-OCT-2000
                                                                                                                                                                                                                                                                                              AAG08681 standard; Protein; 126:AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ValSerGlyAsnLeuGlnLeuAlaGlyGluGluHisAlaLeuLysPheSerGlnMetPhe
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122 SerTrpArg 124
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Search completed: June 24, 2003, 19:31:07 Job time: 58.8062 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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3.9 328	3.9 119	3.9 756	. 3.9 517	3.9 50	3.9 45	2	3.9 23	2	4.0 150384	4.0 1503841	4.0 150384	4.0 8911	4.0 876	4.0 422	4.0 422	4.0 4059	4.0 482	4.0 5881	4.0 190	4.0 1907	4.0 190	4.0 1907	4.0 1294	4.0 684973	4.0 5512
5 9 US-09-986-480-29	4 10 US-09-834-975-840	9 U	7 10 US-09-919-580-874	12	7. 9 US-09-918-995-11773	10 US-09-864-761			10	41 10 US-09-795-668-1	1 9 U	12	9	1 9 US-10-105-891-70	9	12	2 10 US-09-864-761-1571:		9	7 9 US-10-000-489-53	9	7 9 US-09-924-340-53	4 9 US-09-938-842A-4254	3 10 US-09-263-959-1	2 9 US-10-239-676-150
Sequence 29, Appl	Sequence 840, App	Sequence 392, App	Sequence 874, App	Sequence 14, Appl	Sequence 11773, A	Sequence 31695	Sequence	Sequence 7902, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 10019, A	Sequence 70, Appl	Sequence 70, Appl	Sequence 47, Appl	Sequence 15713, A	Sequence, 81, Appl	Sequence 53, Appl	Sequence 53, Appl	Sequence 53, Appl	Sequence 53, Appl	Sequence 4254, Ap	Sequence 1, Appli	Sequence 150, App

ALIGNMENTS

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Sequence 394, A
Patent No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 394
LENGTH: 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
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NAME/KEY: SITE
LOCATION: (15)
                                                                                                                                                                                                                                                                                                                       LOCATION: (7)
OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or c
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                                                        OTHER INFORMATION:
                                                                                           NAME/KEY: SITE
                                                                                                             OTHER INFORMATION: n equals a,t,g,
                                                                                                                              NAME/KEY: SITE LOCATION: (837
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FORMATION: n equals a,t,g,
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANC
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILLING DATE: 2001-03-01
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                                                                                                                                                              Sequence 4160, Application US/09796692 Publication No. US20020198362A1
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Best Local Similarity
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        RIOR APPLICATION NUMBER:
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                                                                   ND METHODS FOR THE DETECTION, MALIGNANCIES
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US-09-796-692-4160
                                                                                      Sequence 4160, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
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Best Local Similarity
Matches 318; Conserv
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SEQ ID NO 4160
      APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Hematological Malignancies
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FILING DATE: 2000-08-07
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FILING DATE: 2000-03-17
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llarity 100.0%;
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Pred. No. 2.8e-94;
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                                                                 Sequence 1201, Application Patent No. US20010055596A1
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                                                  GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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PPLICANT:
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                                 Meagher, Madeleine
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    King, Gordon E.
                   Xu, Jiangchun
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ilarity 100.0%;
Conservative
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Pred. No. 2.8e-94;
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                                                                                                                                                                                                                                                                 Sequence 393, Application US/09764864 Patent No. US20020132753A1
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FILE R
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SOFTWARE: FastSEQ for Windows Version 4.0
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          OTHER INFORMATION: n ename/KEY: SITE LOCATION: (1380)
OTHER INFORMATION: n e
                                                                                                                                                    Prior application data removed
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                             APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                   FILE REFERENCE: PTZ23
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LOCATION: (1)...(318)
OTHER INFORMATION: n =
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LOCATION: (1379)
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                                                                                                   ORGANISM: Homo sapiens
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Pred: No. 6e-94;
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Query Match

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; ORGANISM: Homo sapiens
US-09-918-995-2901
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Best Local
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2901, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
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                                                                                                                        GAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGGCTGCT
                                            GAGGAGTTTGTCAATGTCTACTACACCACCATGGAT
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US-09-764-864-1682
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; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-6557
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SEQ ID NO 1682
LENGTH: 8918
                                                                                  Matches
                                                                                                              Query Match
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Best Local Similarity 98.9
173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                    Prior application data removed - NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                             TYPE: DNA
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SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: DNA
ORGANISM: Homo sapiens
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2199 GATGAAGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTG 2140
                                                                              al Similarity
152; Conserv
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               GTTCATGATGAAGCCACACCAAGCCAAGCCACGGTCCTTGTTGTCATCTGTGGATCAGTG 406
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lo. US20030073623A1
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                                                                                             Score 113;
Pred. No. 9.
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Pred. No. 5.3e-46;
                                                                                                                                                                                                                                                                               consult PALM
                                                                          Mismatches
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                                                                        DB 10;
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US-09-764-864-1683/c
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US-09-764-864-1683
                                                                                                                                                                                                                                        US-09-918-995-36691/c
US-09-918-995-36691/c
; Sequence 36691, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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SEQ ID NO 1683
LENGTH: 8919
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                   SEQ ID NO 36691
                                                                                                 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756 CURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILLING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 1999-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
                                                                 NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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                                    ENGTH: 415
)RGANISM: Homo sapiens
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, NAME/KEY: misc_feature
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, OTHER INFORMATION: n - A,T,C or G
US-09-799-799-3
                                                                                                                                                                                  RESULT 12
US-09-764-877-3374
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                                                                                                                                          Sequence 3374, Application Patent No. US20020147140A1
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Best Local Similarity
                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/799,799
CÜRRENT FILING DATE: 2001-03-07
                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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Prior application data removed - NUMBER OF SEQ ID NOS: 4031
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                                                                                                                                                                                                                                                                                                                                                                                                      7007 GTGACTTGATTTTGTATCCCTGACCTTGCTAAATTCACATACTAGTTCTGGGAGTTTTGT
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79; Conserv
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Pred. No. 7
                        refer to PALM or file wrapper
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US-10-008-118A-11/c
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US-09-764-877-3374
                                           CURRENT APPLICATION NUMBER: US/09/443,704
CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: 60/109,294
                                                                                                                                                                                                                                Sequence 11, Application US/09443704
Patent NO. US20020066120A1
SENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 11
LENGTH: 1141
              EARLIER FILING DATE: No. US20020066120Alember 20, NUMBER OF SEQ ID NOS: 50
                                                                                      APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                         APPLICANT: Liu, Zhan-Bin
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Shi, June
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LENGTH: 32191
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Best Local Similarity 56.3%;
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PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
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ORGANISM: Glycine max
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APPLICANT: Weng, Zude
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Pred. No. 1.5;
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Pred..No. 6.2;
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-097-065-31
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   Query Match
Best Local
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                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/10097065 Publication No. US20030055236A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIOR APPLICATION NUMBER: PCT/US98/27059
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Score 34.8;
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Mismatches

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531 AGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCAGCCCCTAGC 572

Search completed: June 28, 2003; 03:41:58 Job time : 142.193 secs

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Title: Perfect

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Post-processing: Minimum Match 0%
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1 US-07-689-008-5
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1 US-09-134-001C-1659
1 US-09-147-236-1
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2 US-09-147-236-1
2 US-08-835-099A-5
2 US-08-835-099A-5
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3 US-09-157-349-5
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3 US-08-876-974-2
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Patent No.
Query Match
                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
                                                                                                                                                          REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                       CLONE: PTZ9Pt-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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US-09-813-133A-3

US-09-328-111-454

US-09-378-088A-63

US-08-633-993A-10

US-08-844-188-10

US-09-378-088A-67

US-09-378-088A-67

US-09-378-088A-89

US-09-378-088A-30

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US-09-037-188-3
US-09-285-310-3
US-08-092-817-3
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  Score 41.2;
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Database

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Best Local Similarity 18.7%; Pr
Matches 49; Conservative 100;
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NFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION: (617) 542-5070
                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM FS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERAL INFORMATION:
                                                               STRANDEDNESS:
                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/2 FILING DATE: May 6, 1994
                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDRESSEE
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                                                                                                                                                                 (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 Franklin Street
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                                               linear
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SYSTEM: MS-DOS (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/676,818
08-JUL-1996
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                                                                                                      Query Match
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Best Local Similarity
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                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            NAME: Freeman, John W. REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 04599/004001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS (Version 5.(
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: June 25, 19 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5" D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                        Local
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/3
FILING DATE: May 6, 1994
APPLICATION NUMBER: 08/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                               TELEPHONE:
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3362 CTGTGCGCTCACGAGGCTTTCAACATCATTGAAGCCAGGAAAAAACGACAGCT 3421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E OF INVENTION:
                              148 CTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCG 207
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53.2%;
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Pred. No. 1;
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Pred. No. 1;
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268 AGGACAAGAATCCTTGAGT 286

3422 TTTATTTTCTTATATCAGCATGATCAGAACCAGTCTGAAGAATATGGGGTTATGTGGTGAA 3481

208 TTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTC 267

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LENGTH: 3957 base pairs
                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 393-2000
TELEFAX: (415) 393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 337,194
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ent No. 5268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEULUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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 528 GCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCAGCCCCTAGCTCTGTAG 579
                                                                      468 CACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCA 527
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G DATE: 23-MAR-1990
                                                                                                                         Similarity
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                                     CACCGTGGAACAGCTTCTGGTAGCCCGCCACCGCCTGCGCGGTTCTGGCCCGAACCCGCCA 425
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Three Embarcadero Center
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                                                                                                        0; Mismatches
                                                                                                                       Score 33.6;
Pred. No. 1
                                                                                                                                         DB 1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 9540 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31547
TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 393-2286
TELEFAX: (415) 393-2286
TELEX: 340817 MACPAG SFO
TELEX: 140817 MACPAG SFO
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                                                                                                                                                                                   OTHER INFORMATION
                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                              NAME/KEY:
                                            5488 CACCGTGGAACAGCTTCTGGTAGCCCGCCACCGCCTGCGCGTTCTGGCCCGAACCCGCCA 5429
528 GCTAGTGGGGGGGCAGAGGTCTCTTTGCTTTCATTCAGCCCCTAGCTCTGTAG 579
                                                                        468 CACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCA 527
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Calhoon, Roger D
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     Score 33.6; DB 1;
Pred. No. 3.1;
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                                                                                                                                     Length 9540;
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LICANT: FLEISCHMAN,

Robert D

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Query Match 4.0%;
Best Local Similarity 50.6%;
Matches 81; Conservative
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Best Local Similarity
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                                                                            09-103-840A-1
                                                                                                                                                                                      NUMBER OF SEQ ID NOS: SOFTWARE: Patentin Ve
                                                                                                                                                                                                                          CURRENT FILING DATE:
                                                                                                                                                                                                                                       FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
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                                                                                         ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                 TYPE: DNA
                                                                                                                                                  LENGTH: 4411529
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICATION NUMBER: US/09/103,840A
FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                             INVENTION: DNA SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUBERCULOSIS
                                                                                                                                                                                                                                                                               TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                               laire M.
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                                                                                                                                                                                                                          1998-06-24
                                                                                                                                                                                                                                                                                                                                                                   Robert D.
; Score 33.6; D; Pred. No. 55; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.6;
Pred. No. 55;
                                                                                                                                                                                                                                                                                           FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN ANALYSIS IN MYCOBACTERIUM
                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                  4
 79;
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                                Length 4411529;
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Indels
0,
Gaps
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                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus epidermidis US-09-134-001C-1659
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1659
LENGTH: 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-134-001C-1659/c
sequence 1659, Application US/09134001C
atent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Lynn Doucette-Stamm et al
TYLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TYLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2771455 CGAGGAGTTCCTCAGCGACCCCGAGGTTCCGCCCGCATTGCGCCGGCTGGTGC#CGAGGG 2771514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2771395 ATCGGTGGTGATTGGCCTGTATCCGCACTGGGACATCAGCGAGCAGGGCATCACCGCCGC 2771454
2193 TAATCGTTCTTTTAAAGTTGTAAATTCTTCTACTGTT 2157
                                                                                      2253 ACCTATCATATATTGTATATCTTGTTGTGATTCTTTTTCTAAATGTGTAATTGTATTAAC 2194
                                            732 TAGTTTCCTTTTCAAAGTAGTAAACTTTTCTATTTTT 768
                                                                                                                                520 CTGGGCCAGCTAGTGGGGGGGGGCAGAGGTCTCTTTGCTTC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 ATCAGTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGGCCTCACCCAGCAACACAGTGTGGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGA
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                    58.8%;
                                                                                                                                                                               0
                                                                                                                                                                                                  Pred. No. 2.3
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                               40; Indels
                                                                                                                                                                                                                         Length 2661
                                                                                                                                                                               0
                                                                                                                                                                             Gaps
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; ORGANISM: BAC-F2 contig 3 US-09-078-294-7
                                    Query Match
                    Matches
                   Local Similarity
mes 59; Conser
Conservative
                           3.98;
                   0;
                            Score 32;
Pred. No.
                   Mismatches
                            11;
                                  4; Length 11811;
                   45;
                 Indels
                 0;
                 Gaps
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0,

SEQ ID NO

TYPE: DNA

LENGTH: 11811

CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29

PatentIn

Ver.

CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13

Sequence 7, Application US/09078294 Patent No. 6265211

ENERAL INFORMATION:

APPLICANT: Choo, Kong-Hong APPLICANT: Du Sart, Desiree

Kong-Hong Andy

APPLICANT: Cancilla, Michael R.

REFERENCE: Davies Co.

TLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

-09-078-294-7

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                                        RESULT 11
US-09-147-236-10/c
GENERAL INFORMATION
              Patent No.
                         Sequence 10,
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                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, OTHER INFORMATION: c
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ent No. 6316
                                                                                                                                                                                                                                                                                                                                                            OCATION: (12448)..(14652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LICANT: HAYASHI, Takahisa
LE OF INVENTION: NOVEL GENE, GROUP OF GENES,
E REFERENCE: 6537-011-0PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LICANT: TSUCHIDA, Takayasu
LICANT: YOSHINAGA, Fumihiro
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E/KEY: CDS
ATION: (3101)..(5368).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E/KEY: CDS
ATION: (869)..(1891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANISM: Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4379
                                                                                                          8207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T APPLICATION NUMBER: US/09/147,236A
T FILING DATE: 1999-04-08
R APPLICATION NUMBER: PCT/JP97/03633
                                                                                                                                                                                                468 CACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCCTTCCGCTTCCAGGACTGGGCCA
                                                                                                                                         528 GCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCAGCCCCTAGCTCTGTAGA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16836
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(11764)..(12231)
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(7784)..(11761)
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(5373)..(7778)
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                                                                                                                                                                      CACCGTGGAACAGCTTCTGGTACCCCGCCACCGCCTGCGCGCGTTCTGGCCCGAACCCGCCA
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                                                                                                          Application US/09147236A
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                                                                                                                                                                                                                                                   54.9%;
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                                                                                                                                                                                                                                                 Score 31.4;
Pred. No. 22;
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                      51;
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                                                                                                                                                                                                                                                                   Length 16836;
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                                                                                                                                                                                                                                       Gaps
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US-08-946-026-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             nt No.
                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-04-08
CARLIER APPLICATION NUMBER: PCT/JP97/03633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HAYASHI, TAKAhlisa
NITLE OF INVENTION: NOVEL GENE, GROUP OF GENES,
FILE REFERENCE: 6537-011-0PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARLIER FILING DATE: 1997-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Nucleotide sequence is the same as SEQ ID NO:1
                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                          CURRENT APPLICATION DATA
                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
         REGISTRATION NUMBER:
                                                                                     APPLICATION NUMBER: FILING DATE: 07-OC:
                                                                                                                                                                                                                                                                                                                                                                                                                  LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8267 CACCGTGGAACAGCTTCTGGTACCCCGCCACCGCCTGCGCGGTTCTGGCCCGAACCCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 CACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCCTTCCCAGGACTGGGCCA
                                                                                                                                                                                                                                                                                                     Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCAGCCCCTAGCTCTGTAGA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1891)..(2922)
                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08946026
                                                                                                                                                                                                                                                                                                                     E: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Twardzik, Daniel
David J. 31,392
                                                                               NUMBER: US/08/946,026
07-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n at positions 15741 and 15767 may be a, g, c, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                    AND IMMUNODIAGNOSIS
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                  AND METHODS FOR IMMUNOTHERAPY
DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                         701
                                                                                                                                                                                                                                                                                                                         Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51,
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INFORMATION
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                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                              NFORMATION FOR SEQ ID NO:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
                                                                                                                                                                                                    NAME: RESISTATION NUMBER: 34,235
REGISTRATION NUMBER: 47
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 9710:
FILING DATE: 03-APR-1997
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
                                                                                        TOPOLOGY:
                                                                                                    STRANDEDNESS: double
                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 04-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                           TELEFAX: 617-523-6440
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oh 3.7%;
L Similarity 55.7%;
59; Conservative
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                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3114 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NISHI, Kaznori
                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ for Windows Version 2.0
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58.7%;
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            Score 30.8;
Pred. No. 10
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Pred. No. 9
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                          DB 2; Length 2109;
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Best Local
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                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47:
REFERENCE/DOCKET NUMBER: 47:
REFERENCE/DOCKET NUMBER: 47:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                   374 ACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTGAGGGGAACAACAACGGGAC 433
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TTGGGCCGGGATTTCTTCCTGGCCTACCAGCCCTCAGCCCCGCACCA 1393
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PENTION: NOVEL PROTEINS, THEIR PRODUCTION
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IBM Compatible
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ER: 47342
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                                                                                                                    Score 30.8; [Pred. No. 10; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTS & CUSMAN,
                                                                                                                                                 DB
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                                                                                                                                               Length 2109;
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Search completed: June 28, 2003, 03:36:22 Job time: 53.3644 secs
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SEQUENCE CHARACTERISTICS:
LENGTH: 2136 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                          Query Match 3.7%;
Best Local Similarity 55.7%;
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/835,099A FILING DATE: 04-APR-1997 CLASSIFICATION: 514 PRIOR APPLICATION DATA: 083649/1996 FILING DATE: 05-APR-1996 APPLICATION NUMBER: 97105508;2 FILING DATE: 03-APR-1997 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DIKE, BRO
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STATE: MA
STATE: MA
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                                                                              1375 TIGGGCCGGGATTICTICCIGGCCTACCAGCCCTCAGCCCGCACCA 1420
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FTWARE: FastSEQ for Windows Version 2.0
ENT APPLICATION DATA:
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P: 02109
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ENTION: NOVEL PROTEINS, THEIR PRODUCTION
ENTION: AND USE
QUENCES: 18
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Pred. No. 10;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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em_htg_pln:*
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10761.067 Million cell updates/sec
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SUMMARIES

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ALIGNMENTS

VERSION KEYWORDS	ACCESSION				DEFINITION	LOCUS	HSJ322G13	RESULT 1
AL096677.21 GI:10862836 HTG; CpG island; CST8; cys	ESTs, STSs, GSSs and six C AL096677	(SNAP-beta), a novel gene another novel gene for a	genes, the gene for beta-so	(NXT1), a gene for zinc fi	Human DNA sequence from cl	HSJ322G13	v	
cys	, O	a p	a-s) fi	រុំជ	1121		

Pred. No.

is the number of results predicted by chance to have a

SOURCE

attachment protein; NTF2; NXT1; SNAP; zinc finger protein. human. 12180 bp DNA linear PRI 19-MAR-2001 c.lone Rp3-322G13 on chromosome the gene for NTF2-related export protein finger protein FLJ21794, two putative novel a-soluble NSF attachment protein e-for a protein similar to cystatin, a protein similar to cystatin 8 (CST8), x CpG islands, complete sequence.

	/note="Alusx repeat: matches 138282 of consensus"	rebear_red ron			/nore="14 repeat; matches 26/92/40 of consensus" _feature	misc
	MER					repe
		repeat_region	-		repeat_region 3/2/4165 /note="LTR2 repeat: matches 1449 of consensus"	repe
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	Inote-"MIT11 Temest: matches 125 364 of consensus"	repeat_region			/clone_lib="RPCI-3"	
	3		·		/clone="RP3-322G13"	-
		repeat_region			/map="p11.21-12.3"	
	/note="Alusq/x repeat: matches 128259 of consensus"	repeat_region			/db_xret="taxon:9606"	
			-	•		
	278	repeat_region			ce 1. 112180	FEATURES
	10220. 10271 /pote="26 comies 2 mer to 98% conserved"	repeat_region			20	
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	or consensus	repeat region		For	the library RPCI-3 constructed by the group of Pieter de Jong.	
	Something a go of	repeat_region			assembly was confirmed by restriction digest. RP3-322G13 is fro	
	"match: ST	. !			one plasmid subclone or more than one M13 subclone; and the	
❖.	complement (9828. 9960)	misc feature	-	7 5	30); an attempt was made to resolve all sequencing problems, su	
	LVWNGNAVSGQESLSEFFEMLPSSEFQISVVDCQPVHDEATPSQTTVLYVICGSVKFE			÷ i	chemistry or covered by high quality data (i.e., phred quality	
	/translation-"MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTAT	-		ite	regions were either double-stranded or sequenced with an alternate	
	/db_xref="GI:10862837"				sequence was finished as follows unless otherwise noted: all	
	/product="dJ322613.1 (Nif2"Tetaced export process wass)			rue	and of clone RP3-333B15 is at 28739 in this sequence.	
		-			sequence is the entire insert of clone RP3-322G13 The	
		:			Mapping Group. Further information can be found at http://www.sander.ac.uk/MGP/Chr20	
	/note="match: proteins: Tr:Q9UKK6 Tr:Q9UKK6 Tr:Q9UV39 Tr:Q9U342"				chromosome 20, constructed by the Sanger Centre Chromosome 20	
	1/322613.1"				was generated from part of bacterial clone contigs of human	
	/note="Alusx repeat: matches 1292 or consensus"	. CDs	,		on the WORMPEP database can be found at	
	3841.	repeat_region		Ď	Em:, EMBL; Sw:; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information	
	/note="MER2 repeat: matches 994 of consensus"	Tebear_Teaton		TOn.	The following abbreviations are used to associate primary accession	٠
	/note="MIR repeat: matches 220235 of consensus"	3				
		repeat_region		ith	ling to the overlapping clone, a	
	/note="MER2 repeat; matches 1341 of consensus"	repear_region		Ō	together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission	
•	<pre>/note="MIR repeat: matches 99220 of consensus" 7160 7507</pre>			*	lifferences are found these are annotated as variations	
		repeat_region		Ġ.	During sequence assembly data is compared from overlapping clones	COMMENT
	match: ESTS: Em:k33341 Em:kAk223203 Em:kM2431/0 /evidence=not experimental				quests: clonerequest@sanger.a	COMPAND
	"match: cDNAs: Em:AF156957				UK. E-mail enquiries: humquery@sanger.	,
	<pre>/yene= ub322013.1 (NTF2-related export protein NXT1)*</pre>				Direct Submission Sanger Centre, Hinxton, Cambridgeshire,	JOURNAL
	join(60676275,91959991)	mRNA			Lovell, J.	AUTHORS
	Join(606)62/3,91939991) /gene="dJ322G13.1"	gene		•	Mammalia; Eutheria; Primates;	Section Sectio
	not_experimen				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E	0.000
	/note="CpG island"		_		Homo santens	ORGANISM

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                                 CACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTGAGGGGAA
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                                                                                 GTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATGATGAAGC
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   CACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTGAGGGGAA
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match: ESTs: Em:AA417107 Em:R68950 Em:AI023363 Em:AI217180 Em:AKW921034 Em:AA4417012 Em:R68950 Em:AI117089

Em:AKW921034 Em:AA4417012 Em:AA701588 Em:AW019926 Em:AI145986 Em:AW079910 Em:AI961159 Em:AW019926 Em:AA035213 Em:AW082641 Em:AW594742 Em:AA935213 Em:AW7082641 Em:AW594742 Em:AAV236342 Em:AA1984655 Em:AA273573 Em:AA173862 Em:AV236342 Em:AW144279 Em:AL135710 Em:AA365129 Em:AA346014 Em:AA365926 Em:AL1046380 Em:AA2554007 Em:T85404 Em:AA383356
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complement(18864...1928)
/note-match: GSS: Em:AQ145317"
18914...18973
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Em:X60155 Em:X82125 Em:U66561 Em:Af027146 Em:L36315 
Em:M36514 Em:X12592 Em:X64413 Em:AF022158 Em:L75847
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/note="match: GS
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isoform 3)"
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                                                                                                                                                                                                                                        Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                           Clone distribution:
                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
IMAGE: 3450767,
                                                             passed
                                                                                             Series: IRAK Plate:
                                                                                                          through the I.M.A.G.
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Contact: MGC help desk
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Mammalia; Eutheria;
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/organism="Homo sapiens"
/db_xref="LocusID:29107"
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TAGAGACTCTGATTCTGGAAATTCTGACAAATAATTTAATAATACACATG
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1176 bp. mRNA linear NTF2-related export protein 1, clone, mRNA, complete cds. inear PRI 12-JUL-2001 clone MGC:4978

Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom Genome

Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalon@bcm.tmc.edu. Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, Muzny,D.M., Gibbs,R.A. , Lu, , x., Garcia,

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e distribution: MGC clone distribution information can be folugh the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.goves: IRAK Plate: 3 Row: p Column: 18 clone was selected for full length sequencing because it ed the following selection criteria: matched mRNA gi: 7019470 Location/Qualifiers found

BASE CO

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Matches Query Match Best Local

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                                                     CTATTTTTCTACTTGCCCCAGTAGAGACTCTGATTCTGGAAATTCTGACAAATAATTTAAT
                                                                                                                                                                                                                                                    GAAATGCAAACCTCGACTCTCAAGGATGTGAGGAACACAAGTTCATTTCTGTTGTTGCGG
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                                                                                            AGACACTGCAGACTCCACTGTGCCGAGGTTGAACTCTTTTTTGTTGCTCAAGTTCTAGGA
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LVWNCRAVSGGESLSEFFEMLPSSEFQLSVVDCQPVHDEATPSQTTVLVVICGSVKFE
GNKQBDFNQNFILTAQASPSNTVWKIASDCFRFQDWAS"
309 c 316 g 257 t
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/tissue_type="placenta, chorioc
/clone_lib="NIH_MGC_10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="NTF2-related export protein
/protein_id="AAH03410.1"
/db_xref="GI:13097318"
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Pred. No. 6.5e-213;
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Matches 761
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Black, B.E., Levesque, L., Holaska, J.M., Wood, T.
Identification of an NTF2-related factor that
regulates nuclear protein export
Mol. Cell. Biol. 19 (12), 8616-8624 (1999)
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Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete
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Mammalia; Eutheria;
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TTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGC
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GNKQRDFNQNFILTAQASPSNTVWKIASDCFRFQDWAS"
1 265 c 263 g 230 t
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272. .694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="stimulates nuclear protein export"
/note="similar to the sequence presented in GenBank
Accession Number AAA85905; nuclear transport factor
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="NTF2-related export
/protein_id="AAD54942.1"
/db_xref="GI:5880865"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTAT/
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                                                                                                                                                                                                                                                                                                                                                                     Score 759.
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X:, Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                        Direct Submission
Submitted (05-FEB-2001)
Gene Collection (MGC), (
Institute, 31 Center Dr.
                                                                                                     Gaithersburg, Maryland; Web site: http://
                                                                                                                           DNA Sequencing by: Nation Sequencing Center (NISC),
                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
IMAGE:3608037,
                                                                                                                                                                                                                                                                                                                                                                                   BC002687,1
                                                                                                                                                                                                                  NIH-MGC Project URL:
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                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                    Library Preparation: Rubin Laboratory
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramur
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Cancer Genomics Office, National Cancer
rive, Room 11A03, Bethesda, MD 20892-2590,
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through the I.M.A.G.E. Consort
Series: IRAL Plate: 12 Row: m of
This clone was selected for
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/protein_id="AAH02687.1"
/protein_id="AAH02687.1"
/db_xref="cl:12803703"
/translation="MASVDFKTYVDQACRAAEEEVNVYYTTMDKRRRLLSRLYMGTAT
/translation="MASVDFKTYVDQACRAAEEEVNVYYTTMDKRRRLLSRLYMGTAT
/translation="MASVDFKTYVDQACRAAEEEVNVYYTTMDKRRRLLSRLYMGTAT
/translation="MASVDFKTYVDQACRAAEEEVNVYYTTMDKRRRLLSRLYMGTAT
/translation="MASVDFKTYVDCQPVHDEATPSQTTVLVVICGSVKFE
GNKQRDFNQNEILTAAASSSNYTWKIASDCFRFQDMAS"
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/clone_lib="NIH_MGC_44"
/lab_host="DH10B-R"
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/db_xref="LocusID:29107"
/db_xref="taxon:9606"
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erlin Garland, Ran Guin, Letticia Haiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                   through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.oseries: IRAL Plate: 9 Row: p Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 701
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Co DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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IMAGE:2820775,
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               'translation="MASVDFKTYVDQACRAAEEFVNYYYTMDKRRRLLSRLYMGTAT
LVWNGSAVSGGESLSEFFEMLESSEFQJSVVDCQPVHDEATPSGTTVLVVICGSVKFE
GNKQRDFNQNFILTAQASPSITVWKIASDCFRFQDWAS"
263 c 256 g 224 t
                                                                               /product="NTF2-related export protein
/protein_id="AAH03029.1"
/db_xref="GI:12804339"
                                                                                                                                                                                  /tissue_type="Lung, small
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                 codon_start=1
                                                                                                                                                               'note="Vector: pOTB7"
                                                                                                                                                                                                                                    /clone="MGC:4329 IMAGE:2820775"
                                                                                                                                                                                                                                                     /db_xref="LocusID:29107"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Primates; Catarrhini; Hominidae;
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The I.M.A.G.E. Consortium (LLNL)
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IMAGE: 2820775,
BC000759
 Strausberg, R. Direct Submis
                                                                               Homo sapiens.
                                            Mammalia;
                                                               Eukaryota;
                             karyota; Metazoa;
mmalia; Eutheria;
(bases 1 to 972)
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281 TTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGC
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Primates;
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Pred. No. 1.2e-197;
0; Mismatches 8;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
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    TCAGTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCC
                                               TCAGTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCC
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LVWNGNAVSGQESLSEFFEMLPSSEFQISVVDCQPVHDEATPSQTTVLYVICGSVKFE
GNKQRDFNQNFILTAQASPSNTVWKIASDCFRFQDWAS"
265 c 261 g 224 t
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/protein_id="AAH00759.
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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"_
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/db_xref="LocusID:29107"
/db_xref="taxon:9606"
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NTF2-related export pr
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA till insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                              Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Scientification of Tokyo, Laboratory of Genome Structure Analysis, Renome Center; Shirokane-dai, 46-1, Minato-ku, Tokyo 108-8639 Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                        Japan (E-mail:cdnal@ims.u-tokyo.ac.jp,
Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                      University of Tokyo (partly supported
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/tissue_type="human small intestine
/clone_lib="HSI"
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                                                                    /organism="Homo sapiens"
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7 Homo sapiens (NXT1) mRNA"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 GAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
736; Conser
                                                                                                                                                                       Complete
AL354809
                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 135619)
                                                                                                                                  HTG
                                                                                                                                                                                                                Human DNA sequence from clone
                                                                                                                                                   AL354809
                                                                                                                                                                                                                                      AL354809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCCTGTTCATGATGAAGCCACCACCAGCCAGACCACGGTCCTTGTTGTCATCTGTGGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTGCAGCCCCTGGTTCCCCAAGGCAGAGGAAATACCCTGGTGGAGCCCTCCTTCCATA
                                                                                                                                                                                                                                                                                                                                     CTATTTTCTACTTGCAAAAAAAAA 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATTTTTCTACTTGCCCAGTAGAGA 786
                                                                                                                                                                                                                                                                                                                                                                                                                      GTCCCTTTCCTGAATATATACTTGTTTGTCATAGTTTCCTTTTCAAAGTAGTAGAACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAATGCAAACCTCGACTCTCAAGGATGTGAGGAACACAAGTTCATTTCTGTTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGCCTCACCCAGCAACACAGTGTGGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGTGAAGTTTGAGGGGAACAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCCTGTTCATGAAGCCACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCCTTTCCTGAATATATACTTGTTTGTCATAGTTTCCTTTTCAAAGTAGTAAACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                   . 12
                                                                                                                                                                                          sequence.
                                                                                                                                                   GI:13161606
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98.7%;
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Pred. No. 1.2e-193;
0; Mismatches 8;
                                                                                                                                                                                                            135619 bp DNA linear PRI
m clone RP11-527F15 on chromosome
                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
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On Feb 28, 2001 this sequence version.replaced g1:12831820:
During sequence assembly data is compared from overlapping clo
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-527F15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-131F1 is at 135520 in this sequence. The true right end of clone RP11-186J16 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr13
RP11-527F15 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pBACe3.6
                                                                                                                                                                                                 5614. 6265
/note="LIM4 repeat: matches 3331.
                                                                                                                              6368. .6618
/note="MLTIF repeat: matches 1.6619. .7146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (24-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire
                                                                                                        'note="MER1A repeat: matches 2.
                                                                                                                                                                                                                                                                         'note="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MER5B repeat: matches 42. .174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="RP11-527F15"
clone_lib="RPCI-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                  note-"MLT1C repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note "MER7A repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="FAM repeat: matches 1. .168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .135619
                                                                                                                                                                                          te-"match:
                                                                                                                                                                                                                                                                                                                                                                                                te-"MER74A repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                         IPA16 repeat: matches 5418. 6157 of consensus"
                                                                                                                                                                                                                                                                                                                                                       repeat: matches 2289.
                   repeat: matches 1.
                                                                                                                                                                                          STS:
                                                                                                                                                                                          Em:G53026"
                                                                 matches
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                                                                 255.
                       .302 of
                                                                                                          .527 of: consensus
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                                                                                                                                                                                                                                                                                                                  .466 of consensus
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	/note="Alux repeat: matches 223296 of consensus"	repear_region
	note-"TIG	
	note="Alud	eneat regi
	2 repeat: matches 218446 of consens	repeat_region
	5743521	repeat_region
	13343256 13343256	repeat_region
	31. 43032	repeat_region
	to- Marianta Conservat. Her greet took conservat.	repeat_region
	59. 42086 repeat: marches 50/trt or consenses	repeat_region
	1142058	repeat_region
	02 .41949 02 .41949 03 .41949 Conserved"	repeat_region
	5340305 te="MLT2B repe	repeat_region
	92343952 note="MLT2E	repeat_region
	note="L2	, i
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	te="Alusq repeat: matches 1303 of consens 3331624	at_re
	-"L2 repeat: matches 26202710 of consensu 28610	eat_re
	53. 27242	repeat_region
	7043. 27129	repeat_region
	923. 26986 943. 26986	repeat_region
	485524958 ************************************	repeat_region
	377124574 note="IlMC3 repeat: matches 54336	repeat_region
	/323/6 te="L1MC3	repeat_region
	te-"AluJ	
	e-"AluJ 4 2296	, ,
	te="L1MC3 252279	epeat r
	ote="MIR 102226	peat_r
*	<pre>te="LIM4 repeat: matches 44375313 of conse 3921003</pre>	peat_region
	<pre>ce="L2 repeat: matches 26412744 of consensus" 7519945</pre>	
	32. 18430	cepeat_region
	"Lz repeat: matches 26432694 or consensu	epeat_region
	3716488	epeat_region
	70. 14948	epeat_region
	94813260	epeat_region
	62412694 ote="MER21B repeat: matches 716787 of cons	epeat_region
	5 . B repeat: matches 100660 of	repeat_region
	rt .	

61.3%; Score 508.4; DB 9; Leng	Query Match
<pre>13 repeat: matches 3146 of conse</pre>	repeat_region
.54022 "LlME repeat: matches 5305	repeat_region
repeat: matches 1301 of cons	repeat_region
/note="L1ME3 repeat: matches 50605374 of consensus"	repeat_region
/note="FAM repeat: matches 1165 of consensus"	repeat_region
i.	repeat_region
<pre>/note="THE1B repeat: matches 1, .364 of consensus" 51980, .52081</pre>	repeat_region
repeat: matches 58835952	repeat_region
.51618	repeat_region
.50777	repeat_region
=	1000001100101
<pre>/note="AluJo repeat: matches 1282 of consensus sosso so777</pre>	repeat region
er aa 83% conserved"	repeat_region
beat: matches	repeat_region
50321	repeat_region
.47684 117 of	repeat_region
.46620 "L2 repeat: matches 25862677 of	repeat_region
4642446491 /note="L2 repeat: matches 25812652 of consensus"	repeat_region
-	repeat_region
-	repeat_region
=	repeat_region
=	repeat_region

Bes Mat	Best Local Similarity 95.8%; Pred. No. 2.1e-133; Matches 544; Conservative 0; Mismatches 21; Indels 3; Gaps	2;
Qy	207 GITTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGCCAATGCTGTTT	r 266
Db	102025 GTGCACTGTCCCGCCTGTACATGGGCACAGCCCAGGCCTGGTCTGGAACGGCAATGCTGTTT	T 102084
Qy	267 CAGGACAAGAATCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCA	A 326
Дb	102085 CAGGACAAGAATCTTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCA	A 102144
Q.	327 GCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCAGACCACGGTCCTTG	386
Вb	102145 GCGTGGTAGACTGTCAGCCTGTTCATGATGAGCCACAATGAGCCAGACCACGGTCCTTG	3 102204
Qy	387 TTGTCATCTGTGGATCAGTGAAGTTTG-AGGGGAACAACAACGGGACTTCAACCAGAAC	2 445
Db	102205 TIGTGATCTGTGGATCAGTGAAGTTTGAAGGGGAACAAACAA	0 102264
Qγ	446 TTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGC	505
Db	102265 TICATCCTGACCGCCCAGGCCTCACCCAGGAATACAGTGTGGGAAGATCGCAAGTGACTGC	102324
Qγ	506 TTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCA	G 565
B.	102325 TTCCGTTTCCAGGACTGGGCCAGCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCA	G 102384
VQ	566 CCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCAAGGATGTGAGGAACACAAGTTCA	A 625

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REFERENCE.
AUTHORS
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ORGANISM
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AL513495
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                                                                                                                                                                                                                                                                                                                                                                           Insert size: 145810; sum-of-contigs
Insert size: 162901; agarose-fp
Quality coverage: 3.13x in Q20 bases; sum-of-contigs Quality
coverage: 2.95x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 138138 bases at least Q40 Consensus quality: 141205 bases at least Q30 Consensus quality: 141205 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL513495 147310 bp DNA linear HTG 13-JUN-2001 HOMO Sapiens chromosome 13 clone RP11-466M19, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Sanger Centre
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Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                 runs of N, but the exact
This record will be updat
                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between
                                                                                                                                                                                                                                                                                                             consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                   soon as it is available and
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56: contig of
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f 11296 bp in length
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10932 bp in
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                                                     BASE COUNT
ORIGIN
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Query Match
Best Local Similarity
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19912 124426: contig of 4515 bp
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/db_xref="taxon:9606"
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ragment_chain:3"
4915. .78856
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ragment_chain:1"
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ragment_chain:1"
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agment_chain:2"
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ragment_chain:2"
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74814: contig of
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119811: cont
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137019: contig of 12493 bp in length
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65299: contig of
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Score 508.4; DB 2; Pred. No., 2.1e-133;
                                                                                                                   ly_fragment:00307
                                                                                                                                                                                                                                                                                    ly_fragment:00290"
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ACCESSION
VERSION
KEYWORDS
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Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.
                                                                                                                                                                                                1 (bases 1 to 186415)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Barbaria, J., Benton, J., Briava M., Brown, E., Brown, M., Bryant, N.P.
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Rattus no
                                                                                                                                                                                                                                                                                                                                                                                   AC110699
AC110699.3 GI:21744668
HTG; HTGS_PHASE1.
                                                                                                                                                                                 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Brya
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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4 unordered pieces.
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PROGRESS
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Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department Submitted (17-JUL-2002) Human Genome Sequencing Center, One of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 13, 2002 this sequence version replaced gi:18767328.
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Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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REFERENCE
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AUTHORS
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TITLE
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MEDLINE
PUBMED
                 Query Match
Best Local Similarity
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Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                             Charlottesville, VA 22908 USA Sequence update by submitter On Dec 7, 2000 this sequence version Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-DEC-2000) Center for Virginia, 7161 Hospital West, Box Scharlottesville, VA 22908, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Black, B.E. and Paschal, B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulates nuclear protein export
Mol. Cell. Biol. 19 (12), 8616-8624 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Black, B.E., Levesque, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF156958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virginia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLACK, B.E., Levesque, L., Holaska, J.M., Wood, T.C. and Paschal, B.M. Identification of an NTF2-related factor that binds Ran-GTP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTGTTTCTGGAAATTGACAAATAAA 161063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTCTGATTCTGGAAATTCTGACAAATA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTTGAACTCTTTTTTGTTGCTCAAGTTCTAGGAGTCCCTTTCCTGAATATATACTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 644) ick, B.E. and Pasc ect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 644)
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                                                                                       - /translation="MASVDFKTYVDQACRAAEEEVNVYYTTMDKRRRLISRLYMGTAT
LVWNGNAVSGQESLSEFFEMLPSSEFQISVYDCQDVHDDATPSQTTVLVVICGTVKFE
GNKQRDFNQNFILTAQAFSSNTVWKILSDCFRFQDWAS".
168 c 192 g 134 t
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sville, VA 22908,
                                                                                                                                                                 /protein_id="AAD54943.2"
/db_xref="GI:11597238"
                                                                                                                                                                                                                                         Ran-GTP"
                                                                                                                                                                                                                                                         /function="stimulates nuclear protein export"
/note="similar to the sequence presented in GenBank
Accession Number AAA85905; nuclear transport factor;
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                     'product="NTF2-related export
                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                     /gene="NXT1"
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                 45.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paschal, B.
Score 381.2; DB 1
Pred. No. 2.3e-97;
0; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               West,
08, USA
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export protein
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Sciurognathi; Muridae;
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577 Health Sciences Center,
                                  DB 10;
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; Murinae; Mus
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) mRNA, complete
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AC128310.
                                                                                                                                                                                                                                                                                       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
                                                                                                      Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
                                                                                                                                                                              Cleveland.C.D., Cox.C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan_Rocha,S., Durbin,K.J.,
                                                                                                                                                                                                                                                     Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
                              Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
               Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
                                                                                                                                                           Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,J., Li,Z., Lichtarge,O., Lieu,C.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,N.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Mei,G., Metzker,M.,
Meador,M., Morgan,M., Morris,S.,
Mawhiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S.,
Morris,S.,
Mawhiney,E., McLeod,M.P., Mohabbat,K., Morgan,M., Morris,S.,
Mayoyen,A., Mguyen,A., Mguyen,A., Mguyen,A., Mguyen,N.,
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Direct Submission
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NOTE: This is a "working draft" sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
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Center clone name: GYDN
Center clone name: CH330-33618
Center clone name: CH330-33618
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 118171 bases at least 040
Consensus quality: 125568 bases at least Q30
Consensus quality: 130285 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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AX261550 GI:16510517
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bondin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Day, C., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Erante, P., Elarg, N., Errante, P.
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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Liczado, R. J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLedd, M.P., Meador, M., Molyen, A., Morris, S.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.; Morgan, M., Morris, S.,
Miner, G., Miner, S., McLedd, M.P., Meador, M., Moyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwckenkwo, S., Oguh, M., Okuuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pikens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tansey, J., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O.,
Wallilams, G., Willianson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wullilams, G., and Glbbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Department on Jul 12, 2002 this sequence version replaced g1:18701275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 153483)
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Direct Submission
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
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                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 58 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                     as soon as it is available and be preserved.
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                                                                                                                                                                                                                                                                                                                Center project name: GMIT

Center clone name: CH230-133N15

Center clone name: CH230-133N15

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329

Consensus quality: 88643 bases at least 040

Consensus quality: 93107 bases at least 030

Consensus quality: 97900 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ project Information
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                             4.7.4. GCAACAGTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGT
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                                                                                                                                                                                                                                       Submitted (05-NOV-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong Shanghai 201203, P. R. China Location/Qualifiers
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens DC9 (DC9) mRNA, complete cds.
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                                                                                                                                       ATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG 413
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                                                       ATGGAAACAAACAATTTCTTCAACCAGAACTTCCTGCTGACTGCTCAGTCCACTCCCA
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Listing first 45 summaries
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-MODEL=frame+_n2p.model -DEV=xlp
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LIST-45 - DCCALIGN-200 - THR_SCART - THR_MAX-100 - THR_SCART 
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; no neuroprotective; antibacterial; virucide; fungicide; op Human novel secreted protein, Seq ID 1181. nervous system disorder; Alzheimer's corneal infection; wound healing; ep hyperproliferative disorder; cer cerebrovascular disorder; cer vulnerary; secreted protein; cerebral ischaemia; angiogenesis; Alzheimer's disease; infection; oc cardiovascular rheumatoid arthritis; cerebroprotective; nootropic; irucide; fungicide; opthalmalogical; disorder; cardiac arrest; infection; ocular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoassays (ELISA). Disorders which are diagnosed or treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives
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                             GAAATACCCTGGTGGAGCCCTCCTTCCATAGAACCAGAGATGGCATCTGTGGGATTTCAAG
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                                                                                               ACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCACC
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GACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAG
                                                                                                                                AGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACCCAAGC 370
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dadditives
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                              haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into cells or tissues expressing PTAM and for diagnosis of PTAM:related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                     proliferative disorders such as cancers, immune disorders, secretory disorders and other conditions associated with abnormal vesicle trafficking, such as allergies, asthma, urticaria and autoimmune
                                                                                                                                                                                                                 preventing or treating a disorder associated with decreased or increaexpression or activity of PTAM. PTAM polynucleotides are useful for diagnosing conditions associated with PTAM. comprising detecting PTAM forming a hybridisation complex, preferably after PCR amplifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protein transport molecule; PTAM; diagnosis; cytostatic; antiarthritic; antiasthmatic; immunosuppressant; antiarteriosclerotic; antiallergic; antidiabetic; antilipaemic; antirheumatic; osteopathic; dermatological; antianaemic; antipsoriatic; hepatotropic; antigout;
                                                                                                                                                                                                biological sample. Diseases prevented, treated or diagnosed include cell
                                                                                                                                                                                                                                                                          regulate protein transport. PTAM proteins and antagonists are useful for preventing or treating a disorder associated with decreased or increased
                                                                                                                                                                                                                                                                                                            antirheumatic, osteopathic, dermatological, antianaemic, antipson hepatotropic, antigout, antiinflammatory and antiHIV activities,
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                                                                                                                                                                                                                                                                                                                                                                                                        AAA08035 to AAA08042 encode the human protein transport-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human protein transport associated polypeptide and polynucleotide useful for diagnosis, prevention and treatment of cell proliferative and secretory disorders such as leukemia, cystic fibrosis
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immune disorder; cell proliferative disorder; secretory disorder;
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PT Primer sets for synthesizing polynucleotides, particularly the 5602 PT full-length cDNAs defined in the specification, and for the detection PT and/or diagnosis of the abnormality of the proteins encoded by the PT full-length CDNAs - XX Claim 6. CTO IN 17767, 25275 to DOM. Enclish
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Claim 8; SEQ ID 17707; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5002 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary trand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are present human cDNA sequences; AAB92446 to AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13633 to AAH13629 and AAH13639 and AAH13639 to AAH13630 to AAH13630 to AAH13630 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 197 AA;

Alignment Scores:				
Pred. No.:	8.82e-59	Length:	197	
Score:	584.50	Matches:	106	
Percent Similarity:	90.85%	Conservative:	23	
Best Local Similarity:	74.65%	Mismatches:	12	
Query Match:	39.25%	Indels:	_	
DB:	22	Gaps:	-	
10-00-763-00-10 (1-020) - 1076-00-763-00-11-1076	01 4 3 505 370	/1 - 107 ¢		٠.

5-09-763-902B-10 (1-830) x AAB95379 (1-197)

0	CC () () () () () () () () () () () () ()	
ΟΥ .	107 GAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAG 163	
Дb	55 GlnMetAlaThrSerLeuAspPheLysThrTyrValAspGlnAlaCysArgAlaAlaGlu 74	
Qy	164 GAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTG 223	
Db	75 GluPheValAsnIleTyrTyrGluThrMetAspLysArgArgArgAlaLeuThrArgLeu 94	
Qy	224 TACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATCCTTG 283	
Db	95 TyrLeuAspLysAlaThrLeuIleTrpAsnGlyAsnAlaValSerGlyLeuAspAlaLeu 114	
Qy	284 AGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGGTTCCAAATCAGCGTGGTAGACTGCCAG 343	
D	115 AsnAsnPhePheAspThrLeuProSerSerGluPheGlnValAsnMetLeuAspCysGln 134	
Qy	344 CCTGTTCATGATGAAGCCACCAACCCAAGCCAGGACCACGGTCCTTGTTGTTGTTCATCTGTGGATCA 403	
B	hrSer	
Qy	404 GTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAG 463	
Db	155 ValLysPheAspGlyAsnLysGlnHisPhePheAsnGlnAsnPheLeuLeuThrAlaGln 174	
Oy :	464 GCCTCACCCAGCAACAGTGTGGGAAGATCGCAAGTGACTGCCTTCCAGGACTGG 523	
Db	175 SerThrProAsnAsnThrValTrpLysIleAlaSerAspCysPheArgPheGlnAspTrp 194	
Qу	524 GCCAGC 529	
7	105 605 105	

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AAY82323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                     Pred
                                                  Alignment Scores
                                                                                                                                                                                                                     diagnosing conditions associated with PTAM, comprising detecting PTAM by forming a hybridisation complex, preferably after PCR amplifying the biological sample. Diseases prevented, treated or diagnosed include cell proliferative disorders such as cancers; immune disorders, secretory disorders and other conditions associated with abnormal vesicle trafficking, such as allergies, asthma, urticaria and autoimmune haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as haemolytic anaemia. Anti-PTAM antibodies may be used as antagonists, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human protein transport-associated polypeptide and pouseful for diagnosis, prevention and treatment of cell proand secretory disorders such as leukemia, cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarthritic; antiasthmatic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 68; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     urticaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; antianaemic;
                                                                                                                                     into cells or tissues expressing PTAM and for diagnosis of PTAM-related disorders. PTAM, its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds. PTAM polynucleotides are useful for generating hybridisation probes useful in mapping the
                                                                                                                                                                                                                                                                                                                                             preventing or treating a disorder associated with decreased or incressors or activity of PTAM. PTAM polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic, antiarthritic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA08035 to AAA08042 encode the human protein transport-associated
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                  regulate protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic, osteopathic, dermatological,
                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic, antiallergic, antidiabetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lmmune disorder; antiHIV; protein transport regulator; cancer;
lmmune disorder; cell proliferative disorder; secretory disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                  hepatotropic, antigout, antiinflammatory and antiHIV activities,
                                                                                                                                                                                                        targeting or delivery mechanism for bringing pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergy; al haemolytic
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 8.57e-59
584.00
91.30%
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Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiasthmatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein transport regulator;
                                                                                                                                                                                                                                                                                                                                                               iinflammatory and antiHIV activities, and
PTAM proteins and antagonists are useful for
sorder associated with decreased or increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vesicle trafficking; asthma;
Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82324. The PTAMS have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic; osteopathic;
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104
22
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proliferative
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RESULT 5
ABB04459
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Query Match:
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Polypeptide-human NTF2 associated protein 16 and encoding it -
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                                                                                                                                                                                                                                                                            CN1313332-A
                                                                                                                                                                                                                                                                                                                                                Human NTF2 associated protein
                                                                 Claim 1; Page
                                                                                       encoding
                                                                                                                          N-PSDB;
                                                                                                                                      WPI;
                                                                                                                                                                                                                              15-MAR-2000;
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                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                          Human; NTF2 associated
                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2002
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DB; ABA05754.
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                                                                                                                                                                                 BODE GENE DEV CO LTD SHANGHAI
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                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAsnLysGlnHisPhePheAsnGlnAsnPheLeuLeuThrAlaGlnSerThrProAsn
                                                                                                                                                                                                                               2000CN-0114918
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                 26(Disclosure); 32pp; Chinese
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39
21
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Indels:
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                                                                                                   polynucleotide
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The present invention provides the protein and coding NTF2 associated protein 16. The sequences can be used cancer and HIV infection, as well as other diseases is the protein of the invention.

d coding

in the treatment o

atment of sequence

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Percent Similarity:
Best Local Similarity:
Query Match:
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 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
                                                                                                                                Homo sapiens.
                                                                                                                                                  cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fingicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; cerebral ischaemia; angiogenesi ocular disorder; hizhelmer's disease; infection; ocular disorder; screen infection; ocular disorder; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                              AAU16227
                                                                 17-JAN-2001;
                                                                                                           WO200155322-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                            Human novel secreted protein,
                                                                                                                                                                                                                                        Human; immunosuppressive; antiarthritic; antirheumatic;
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                                                                                                                                                                                                                                                                                                                                                                    GGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGC
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
                                                                 2001WO-US01341
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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18-APR-2000;
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21-SEP-2
25-SEP-2
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          Claim 11; SEQ ID No 1180; 980pp; English.
The invention relates to isolated nucleic acid
                   New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                           Rosen CA,
                                                                      (HUMA-) HUMAN GENOME
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                                          2001-488783/53.
DB; AAS26214.
                                                           Barash SC,
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                                                                      SCI INC.
                                                           Ruben
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                          and
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molecules and their

Drosophila;

26-MAR-2002

(first entry)

Drosophila melanogaster polypeptide SEQ ID NO 21843

developmental biology; cell signalling; insecticide;

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RESULT 7
ABB65017
ID ABB6
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AC ABB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.
                                                                                                                  ABB65017;
                                                                                                                                                       ABB65017 standard; Protein; 133
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                                                                                                                                                                                                                                                            GTGTGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGC
                                                                                                                                                                                                                                                                                                                                                            AAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukarytes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16173) and the encoded proteins
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL09120.
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GlnLeuArgLysPheGlnGlnThrPheIleValThrAlaGlu
                                 AAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCCAGCAACACA 481
                                                                                                                                       LeuProSerSerAsnHisGinLeuAsnThrLeuAspAlaGinProIleValAspGinAla
                                                                                                                                                                        TTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCC
                                                                                                                                                                                                                                            ValSerAsnGlnLeuAlaTyrLeuIleMetAlaSerGlySerValLysPheAlaAspGln
                                                                                                     ACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTGAGGGGAAC
                                                                                                                                                                                                         LeuSerTrpAsnGlyAsnGlyAlaIleGlyArgGlnMetIleGluSerTyrPheGlnGlu
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(first entry)
                Protein;
                                  132
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; Arabidopsis thaliana protein fragment SEQ ID NO: 11042

2000EP-0301439

9905-0137528 9908-0137502 9908-0137724 9908-0138094 9908-0138540 9908-013819 9908-0139119 9908-0139452 99US-01 9905-013422 99US-0: 99US-0134256 99US-0134218

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990S-0147038.
990S-0147302.
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Pred. No.:
                    US-09-763-902B-10 (1-830) x AAG12073 (1-125)
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86 AGCCCTCCTTCCATAGAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAG 145
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130.00
41.50%
29.25%
8.73%
                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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28-JUL 02-AUG 02-AUG 02-AUG 03-AUG 04-AUG 04-AUG 05-AUG 05-AUG 05-AUG 06-AUG 06-AUG 09-AUG 09-AUG 11-AUG

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			fragment transdu napping;	53 P.P.	CCGCCCAGGCCT	GCCAGCCTGTTC erGlnPro GGATCAGTGAAGT	TACATGGGCACAGCCACCCTGGTCTGGAATGGC ::: :::	::: luGluGluValAlaSe AGGAGTTTGTCAATGT
			D NO: 1 pathwa express		CACCCAGCAAC	CTGTTCATGATGAAGCCACACCAAGCCAGACCACG	CCACCCTGGTC:: :: erLeuLeuThr hAAATGTTGCCT:: ysGlnLeuPro	 SerAla HisTyrTyrHis
:			441. y; metabolic ion control;		ACAGTGTGGA	ATGAAGCCACACCAAGCCAGACCACG erSerMetAlaGlyGlyCysGlyGly erSerMetAlaGlyGlyCysGlyGly AGGGGAACAAACAACGGGACTTC ::: lsGlyGluAspHisProLeuArgPhe	TCTGGAATGGCAAT :: hrPheGluGlyGln CTTCCAGCGAGTTC copheAspGlnCys	ACCATGGATAAGCG
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99US-0147303 99US-0147416 99US-0147493 99US-0147935 99US-0148171 99US-0148319

99US-0149426. 99US-0149722. 99US-0149723.

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3-0153070 3-0153758 3-0154018 3-0154039 3-0154779 02-AUG-1999

990S-0145918. 990S-0145951. 990S-0146386. 990S-0146388. 990S-0146389. 990S-0147038. 990S-0147030. 990S-0147204. 990S-0147192.

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Percent Similarity:
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                                           pharmaceutical.
                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                   26-MAR-2002
WO200171042-A2
                      Drosophila melanogaster
                                                                             Drosophila melanogaster polypeptide SEQ
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                                                                                                                                                                                          ValPheAsnAspIlePheSerTrpArg
                                                                                                                                                                                                                                      SerGlnMetPheHisLeuMetProThrProGlnGlySer-:
                                                                                                                                                                                                                                                            AACCAGAACTTCATCCTG-----ACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAG
                                                                                                                                                                                                                                                                                    MetLeuValPheValSerGlyAsnLeuGlnLeuAlaGlyGluLysHisAlaLeuLysPhe
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99US-0161992.
99US-0161993.
99US-0162142.
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Matches:
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157865

0159638. 0159584. 0160741. 0160767.

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standard; Protein; 690 AA
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Best Local Similarity:
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                                                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                      pharmaceutical
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                                 ABB66052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| :::::: ::: | |||||| |||||||| TyrAsnHisAsnSerSerTyrIleHisGlyGluSerLysLeuValValGlyGlnArgGlu
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Mismatches:
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11-JUL-2000; 2000US-0614150.
                                               23-MAR-2001; 2001WO-US09231
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N-PSDB; ABL11507.
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              27-SEP-2001
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences spenanc. DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 GAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGCGCGTTTGCTGTCCCGCCTG 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 24948; 21pp + Sequence Listing; English.
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               ATCTGTGGATCAGTGAAGTTTGAGGGGAACAAACAACGG----GACTTCAACCAGAACTTC
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                                                                         TCCTTGAGTGAGTTTTTTGAAATGTTGCCT----TCCAGCGAGTTCCAAATCAGCGTG
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99US-0149722 99US-0149723 99US-0149929 99US-0149902 99US-0149930

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-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapext
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                 US-08-836-791-9
US-08-858-207A-301
US-08-856-963-12
US-08-222-616-24
US-08-446-648-24
PCT-US95-04228-24
US-09-413-814-72
US-09-579-181-2
US-08-570-227A-2
US-09-579-121-1
US-08-570-227A-2
US-09-77-991-2
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US-08-836-791-9
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schweighoffer,
APPLICANT: Tocque, Bruno
TITLE OF INVENTION: Peptid
TITLE OF INVENTION: And Protes
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                  APPLICATION NUMBER: FR 9
FILING DATE: 22-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                          FILING DATE: 530 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 19426
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                   APPLICATION NUMBER:
                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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Parker, Fabienne
Schweighoffer, Fabien
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 UMBÉR: FR 95/05753
16-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides Capable of Binding to the GAP Protein SH3 Domain, Nucleotide Sequences Coding Therefor,
                                                                                                                                                     US/08/836,791
                                                                          94/13955
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US-09-336-643A-20
US-08-952-127-12
US-08-943-600A-3
US-08-278-635B-7
US-08-464-258B-7
US-08-464-258B-7
US-08-471-961-7
US-08-941-445A-11
US-08-99-578-2
US-08-725-012-2
US-08-725-012-2
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US-09-763-902B-10 (1-830) x US-08-836-791-9 (1-466)
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                                                                                                                                                                                                                                  Sequence 301, Application US/08858207A Patent No. 6348328
                                                                                                                                                                                                            GENERAL INFORMATION:
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.NEORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
            ADDRESSEE:
STREET: 7:
CITY: Kin
                                                                              PPLICANT: Black, Michael
PPLICANT: Hodgson, John
PPLICANT: Knowles, David
PPLICANT: Nicholas, Richard
PPLICANT: Stodola, Robert
ITLE OF INVENTION: No. 6348328el Compounds
IMBER OF SEQUENCES: 552
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REGISTRATION NUMBER: 35,139
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                          SmithKline Beecham Corporation 9 Swedeland Road
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Best Local Similarity:
Query Match:
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MOLECULE TYPE:
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LENGTH: 671 amino acid
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MEDIUM TYPE: Diskett
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                      495
                                                                                                                                                  487
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                                                                                                                                                                                  266 TCAGGACAAGAATCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATC 325
                                                                                                                                                                                                                      467 AlaThrValGlyTyrLeuGluSerGlyGlnAspArgPheValTyrAsnThrThrProIle
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14-MAY-1996
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                                                                        ProllellelleVallleThrProGlnSerThrGlyProGln 508
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Query Match:

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TOPOLOGY:

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					DNESS: linear	STRANDEDNESS TOPOLOGY: 1	
•			,	12: s	NN FOR SEQ ID NO: 1 CHARACTERISTICS: 1: 498 amino acids amino acid	INFORMATION SEQUENCE C LENGTH: TYPE: 8	44.44.4
					NE: 202-824-8000 : 202-824-8199 248516	TELEPHON TELEFAX: TELEX:	
٠.			٠.	18046.036	REFERENCE/DOCKET NUMBER:	REFERENCE TELECOMMUNI	
	1			ON: Brian P. 32,747	INFORMATI Ighnessy, NUMBER:	ATTORNEY/AGENT NAME: O'Shau REGISTRATION	
		•	٠.	٠.		FILING CLASSIF	
				/08/660,963	ZZ	CURRENT APPLICATION	
			Version #1.30	s-DOS #1.0,	SYSTEM: Patentir	OPERATING SOFTWARE:	·
				tible	TYPE: Floppy disk R: IBM PC compatible	MEDIUM TY COMPUTER:	
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					DOOS .	COUNTRY:	\
					Washington D.C.	CITY: .	٠. ٠.
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					SEQUENCES:	R OF	
		TUITARY	ING OF THE OVINE PITUITARY	LAR CLON	INVENTION: MOLECULAR	TITLE OF	
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				el O.	INFORMATION: PANT: Thorner, Michael	APPLICANT	
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				9 5 5 6 6 7 7 7	2	RESULT 3 US-08-660-963-1	US
	615	HisArgThrTyrLeuPhe	uGluIle	eAlaGlyLeuArgE		596 1	₽.
	727	TACTTGTTT	TCCTGAATATA	TCTAGGAGTCCCTT	TTTTTTGTTGCTCAAGTTCTAGGAGTCCCTTTCCTGAATATA	677 1	δ
	595	GluPheArgArgAla	rgLeuTyrPheGlu	eAsnThrMetAsn <i>F</i>	ThrSerIleLeuLeuPheAsnThrMetAsnArgLeuTyrPheGluGluPheArgArgAla	576 T	밁
	676	GAGGTTGAACTC	GACTCCACTGTGCC	GCGGAGACACTGC	AGTTCATTTCTGTTGTTGCGGAGACACTGCAGACTCCACTGTGCCGAGGTT	620 A	8
	575	ValLeuGlyIleAla	letLeuAlaGlyAla	gGluArgTrpValk	 LeuAspAsnIleGlnArgGluArgTrpValMetLeuAlaGlyAlaValLeuGlyIleAla	. 556 L	밁
	619	GTGAGGAACACA			AAGGAT	. 602 A	80
	555	Ile				4.	당 5
	601		er	IleGluAsnTrpValSer	GlyIleGluAsnTrpValSer	537 G	B
	556	DAGAGGTCTCTTTGC	GCTAGTGGGGGTGGC	CCAGGACTGGGCCA	AGTGACTGCTTCCGCTTCCAGGACTGGGCCAGGTAGTGGGGGGTGGCAGAGGTCTCTTTGC	497 A	Qy
	536	euIleGlnArgGln	erAspAlaGlnGluI	uPheAsnGlnLeuS	ValGlnAsnTyrValLeuPheAsnGlnLeuSerAspAlaGlnGluLeuIleGlnArgGln	517 V	B
	496		CACCCAGCAACACAC	GACCGCCCAGGCCT	AACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCA	437 A	γQ

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RESULT US-08- Patqu Patqu PAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	D 24 D	Qy Qy	Db Oy	Qy Db Qy	OY OY OY	US-09- Qy Db Db Qy	Score: Percent Best Loc Query Ma DB:
OB-222-616-24 -OB-222-616-24 -OB-222-616-24 -OB-222-616-24 -OB-222-616-24 -OB-222-616-24 -OB-222-616-24 -OB-222-616 -OB-222-616-24 -OB-222-616 -OB-222	197 LeuSerGlyGlySerThrAlaProGlyThrThrSerThrProSer	TCGCAAGTGACTGCTTCCAGGACTGGGCCAGCT	405 TGAAGTTTGAGGGAACAAACAACGAGGGACTTCAACCAGAACTTCATCCTGACCGCCC 461	285 GTGAGTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGC 344 113	234CAG 236 80 SerserLeuSerGluArgThrSerLysHisValTyrLysLeuLeuLysGlyCysProThr 99 80 CACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATCCTTGA 284	763-902B-10 (1-830) x US-08-660-963-12 (1-498) 159 CTGAGGAGTTTGTCAATGTCTACTACCACCATGGATAAGCGGC	e: 81.50 Matches: 53 Int Similarity: 33.33% Conservative: 16 Local Similarity: 25.60% Mismatches: 52 Match: 5.47% Indels: 86 Gaps: 10
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Oy 321 AAATCAGCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACCAACCA	1019 201 1031 261 1041	-09-763-902E 33 985 90 1005	Alignment Scores: Pred. No.: 80.00 Percent Similarity: Best Local Similarity: Query Match: 1.43 20.778 Query Match: 1.65	MEDIUM TYPE: 5.25 inch, 360 kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION LDATA; APPLICATION UMBER: US/08/222,616 FILING DATE: 4-APR-1994 CLASSIFICATION LDATA; APPLICATION NOMER: DCT/US93/00586 PRIOR APPLICATION NOMER: O7/826935 PRIOR APPLICATION NUMBER: 07/826935 PRIOR APPLICATION NUMBER: 07/826935 PRIOR APPLICATION NUMBER: 07/826935 FILING DATE: 22-JAN-1993 PRIOR APPLICATION NUMBER: B21P2 TELECOMMUNICATION NUMBER: 821P2 TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994 TELEFAX: 415/952-9881 TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 1276 amino acids TYPE: amino acid
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FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378 REFERENCE/DOCKET NUMBER: p0821p3pCT TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994 TELEPHONE: 415/225-1994 TELEPEN: 910/371-7168 INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 1276 amino acids TYPE: Amino acid TOPOLOGY: Linear	TE 44080 TYPE: DIUM TYPE: MAPTIER: IBM ERATING: SYSIEM ERATION NU LING DATE: LING DATE: ASSIFICATION NU R APPLICATION NU R APPLI	ICANT: IC	RESULT 5 US-08-446:648-24 US-08-46:648-24 Sequence 24, Application US/08446648 Patent No. 6331302 GENERAL INFORMATION: APPLICANT: Genentech, Inc. APPLICANT: Genentech, Exian D. APPLICANT: Genentech, David APPLICANT: Genentech, David APPLICANT: Lee, James M. APPLICANT: Lee, James M. APPLICANT: Lee, James M.	Db 1086 ProTrpValArgSerArgArgProLysArgValLeuProCysGlnLeuGlnSerGlyGly 110 Qy 528 GCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCAGCCCTAGCTCTAAGAAATGC 587

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NERAL INFORMATION:
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LENGTH: 1276 amino aci
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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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CITY: South San Francisco
STATE: California
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Wood, William I
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SOFTWARE: E
            ORGANISM: Sorangium cellulosum 09-413-814-72
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                                                                                                                                               EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
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                                                                                                                                NUMBER OF SEQ
                                                   TYPE: PRT
                                                                                                                                                                                                                     PPLICANT: Reichenbach, Hans
TILE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide
TILE OF INVENTION: heteropolyketide compounds
TLE REFERENCE: PCT/US 99/33535
                                                                                                                                                                                                                                                                                                            PPLICANT: Mueller, Joachim
                                                                                                                                                                                                                                                                                                                                                PLICANT: Brandt, Petra
PLICANT: Cino, Paul M
PLICANT: Dougherty, Brian A
PLICANT: Goldberg, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                            ICANT: Beyer, Stefan
ICANT: Bloecker, Helmut
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                                                                                                                                                                                      APPLICATION NUMBER: US/09/413,814 FILING DATE: 1999-10-07
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US-09-579-181-2
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US-09-579-181-2
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Query Match:
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CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 1999-05-27
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                                                                  1221 LeuAlaProValValProAlaAlaProGlyProProSerLeuGln--
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                          GCCCTCCTTCCATAGAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGG 146
                                                                                                       CTTCAACCTTACTTCCCTGCAGCCCCTGGTTCCCCAAGGCAGAGGAAATACCCTGGTGGA 86
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US-09-579-181-1
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                                   US-09-763-902B-10 (1-830) x US-09-579-181-1 (1-3118)
                                                                                         Query Match:
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Best Local Similarity:
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                                                                                                                                                                                      Alignment Scores
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tent No. 6365372
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   27 CTTCAACCTTACTTCCCTGCAGCCCCTGGTTCCCCAAGGCAGAGGAAATACCCTTGGTGGA 86
                                                                                                                                                                                                                                                                                        3118
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16153-4247
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Indels:
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US-08-570-227A-2
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                                                                                                                                                                                                                                                                                                                                                                                                             general information:
                                       SOFTWARE: FastSEQ Version CURRENT APPLICATION DATA:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
                                                                           OPERATING SYSTEM:
                                                                                                                                                                      COUNTRY:
                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                    E: Schwegman,
P.O. Box 2938
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VENTION: DAR ENCONDING TGF-BETA INDUCIBLE VENTION: EARLY FACTOR-1 (TIEF-1), A GENE I VENTION: BY OSTEOBLASTS
                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                           Subramaniam, M.
                                                                                                 IBM Compatible
 MBER: US/08/570,227A
11-DEC-1995
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US-09-763-902B-10 (1-830) x US-08-570-227A-2 (1-480)
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEPHONE: 612-359-3260
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STRANDEDNESS: sir
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REGISTRATION NUMBER: 3
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RIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                             374 ACCACGGTCCTTGTT---
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                                                        rThrProProSerGlnProProAlaValCysProProValValPheMetGlyThrGlnVa
                                                                                                                                 IleCysGlnMetValProLeuProAlaAsn-AsnProValValThrThrValValProSe
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Matches:
Conservative:
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Indels:
-CCTCACCCAGCAACACAGTGTGGAAGATCGCA 496
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Best Local Similarity:
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EARLIER FILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TGF-Beta inducible early factor-1 TITLE OF INVENTION: (TIEF-1) and a method to detect b: FILE REFERENCE: 150.157US2
CURRENT APPLICATION NUMBER: US/09/077,991
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: PCT/US96/19555
EARLIER FILING DATE: 1996-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spelsberg, T.C.
APPLICANT: Roche, P.C.
TITLE OF INVENTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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      217 ValAlaAspValAspGluLysAlaSerAlaAlaLeuTyrAspPheSerValProSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                       118 HisPheLysSerLeuSerAspThrAlaLysProHisIleAlaAlaPro---PheLysGlu 136
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                                                                                                                                                                                                                                                                                                                                                               65 GCAGAGGAAATACCCTGGTGGAGCCCTCCTTCCATAGAACCAGAGATGGCATCTGTGGAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                             11 CATTCACGTGGCTTCTCTTCAACCTTACTTCCC-----TGCAGCCCCTGGTTCCCCAAG
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                                                                                                                         CGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCT-
                                                                                                                                                             IleLeuAsnTyrGlnAsnAsnSerPheArgArgArgThrHisLeuAsnValGluAlaAla
                                                                                                                                                                                                    TTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTG---
                                                                                                                                                                                                                                                                                      TTCAAGACCTATGTGGATCAGGCCTGCAGA.--
                                                                                 ArgLysAsnIleProCysAlaAlaValSerProAsnArgSerLysCysGluArgAsnThr
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                                           -GTTTCAGGACAAGAATCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGC
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.23.21%
5.24%
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                      --CTGTCC
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밁 S Query Match: DB:

Pred. No.:

TOPOLOGY: 1 MOLECULE TYPE:

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US-08-290-301-82
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Patent No.
                                                                          CLASSIFICATION.

PRIOR APPLICATION NUMBER: FI 943133

APPLICATION NUMBER: FI 943133

FILING DATE: 29 June 1994

FILING DATE: 29 June 1994

FILING DATE: 1993/00049
                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS
SOFTWARE: WP5.1 file exported as DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alko Ltd.
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NITLE OF INVENTION: Increasing the trehalose content increasing the transforming the invention: the structural genes for trehalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                             CLASSIFICATION:
APPLICATION NUMBER: PCT/F193/00 FILING DATE: 15 February 1993 APPLICATION NUMBER: 07/841,997 FILING DATE: 28 February 1992 APPLICATION NUMBER: 07/836,021 FILING DATE: 14 February 1992
                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             COUNTRY: Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 GAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATGAAGCCACACCAAGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                       PO Box 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palva, Tupio
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                                                                                                                                                                                                                                                                        IBM PC/XT/AT
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15 August 1994
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                                                                                                                                                                                                                                                                                           3.5 inch,
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-013-598-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 467-6300
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LENGTH: 1098 amino aci
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HYPOTHETICAL:
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
ADDRESSEE: Alko Ltd.
STREET: PO Box 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
..
       SOFTWARE: WP5.1 file & CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                               TITLE OF
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                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
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                                                                                                                                                                                                                                                                                ITLE OF
                                            OPERATING SYSTEM: PC-DOS
SOFTWARE: WP5.1 file exported as DOS
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6323001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                RY: Finland
SF-00101
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ondesborough,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide
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47.37%
35.53%
5.24%
                                                                                                                                                                                                                                                                                  the structural
                                                                                                                                                                                                                                                                                                 of organisms
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         US/09/013,598
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                                                                                                                                                                                                                                                                                    genes for trehalose
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                                                                                                                                                                                                                                                                                                     them with combinations
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CLASSIFICATION:

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US-09-763-902B-10 (1-830) x US-09-013-598-82 (1-1098)
                                                                                                                                                                                                                                                                          equence 4, Application US/08216260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 466-20 INO:
                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 467-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14 February ATTORNEY/AGENT INFORMATION:
                                                                                      STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                          STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DALL.
APPLICATION NUMBER: 0// 1992
TITING DATE: 28 February 1992
TITING DATE: 1992
TITING DATE: 0797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: NUMBER: PCT/F137, APPLICATION NUMBER: PCT/F137, 193
FILING DATE: 15 February 1993
FILING DATE: 07/841,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 0//830,04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                          ICANT: Minson, Anthony C.
E OF INVENTION: VIRAL VACCINES
ER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                              237 ---SerSerAlaProProSerIleLysArgIleThrProHisLeuThr 251
                                                                                                                                                                                                                                                                                                                                                                             555 GCTTCATTCAGCCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCA 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 ProLysSerArgAlaGlyAsnArgPro----
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Amino acid
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                                                          United States
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                                                                                                                                                                                                                     Inglis, Stephen C.
Boursnell, Michael E.G.
                                                                                                               Flehr, Hohbach, Test, Albritton & Herbert
Attn: Walter H. Dreger
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Conservative:
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Query Match:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/168,643
ETLING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/030,073 FILING DATE: 19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9
FILING DATE: 19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/216,260
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                          115 LeuGlyArgProProAsnAlaSerLeuProAlaProThrThrValGluProThrAlaGln 134
     155 LeuArgSerArgAlaTrpValThr--
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                                                                                                                                                                                                                                                                                          171 TCAATGTCTACTACACCA-----CCATGGATAAGCGGCGGGGTTTGCTGTCCCGCCTGT 224
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                                                                                           -----CCTTGAGTGAGTTTTTTGAAATGTTGCCTT-----CCAGCGAGTTCC-----
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Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:

08-216-260-4

501

ENERAL INFORMATION:

APPLICANT:

ITLE OF

ADDRESSEE:

COMPUTER READABLE

COUNTRY: | ZIP: 9411:

Alignment Scores:

. No.:

-09-013-598-82

MOLECULE TYPE:

TOPOLOGY:

ENGTH:

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NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 766
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-08-846-762-5
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S-08-846-762-5
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PPLICANT: Charter, Deborah
PPLICANT: Charter, Deborah
ITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
ITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
ITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Lam, Joseph S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URRENT APPLICATION NUMBER: US/08/846,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 CCAGCTAGTGGGGGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 LeuAlaThrArgGlyLeuLeuArgSerProGlyArgTyrValTyrPheSerProSerAla 241
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                                                                                                                                                                                                         323 LeuPheIleTrpSerGlyTyrCysValPheSerGlySerGlnAspAlaGlnTyrPheAla 342
363 ArgGluLeuProAlaArgLeuAlaIleLeuAlaGlyLeuLeuGlyAla 378
                                                     356 GAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCA 403
                                                                                                                                                       296 GAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATGAT 355
                                                                                                                                                                                                                                                                                                                 303 LeuPheMetCysLeuProCysArgTrpArgLeuProValPheIleLeuLeuAlaIleLeu 322
                                                                                                                                                                                                                                                                                                                                                           179 TACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCACAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 ProArgAlaGluGluLeuProLeuLeuHisThrCysSerIleAlaAsnGluMet----- 294
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Search completed: June 24, 2003, 19:40:14 Job time: 23.711 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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- FGAPOP=6
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-TRR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTEM-pto -NORM-ext -HEAPSIZE-500 -MINLEN-

-THR_MIN-0 -DO0000000 -USER-US09763902_@CGN_1_1_24_@runat_24062003_130343_12522

-MAXLEN-2000000000 -USER-US09763902_@CGN_1_124_@runat_24062003_130343_12522

-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100

-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDP-10 -XGAPEXT-0.
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-DB-Published_Applications_AA -QFMT-fastan -SUFFIX-n2p.rapb -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-biosum62
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Match Length DB
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1489
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LOCATION: (5) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino NAME/KEY: SITE	LOCATION: (3) OTHER INFORMATION: Xaa NAME/KEY: SITE		ORGANISM: Homo sapiens FEATURE:	TYPE: PRT	SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1181	Prior application data removed - NUMBER OF SEQ ID NOS: 1792 -	CURRENT FILING DATE: 2001-01-17	APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE PERFERENCE 20773	Sequence 1181, Application Patent No. US20020132753A1 GENERAL INFORMATION:	RESULT 1 US-09-764-864-1181
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                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 1180
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                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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SEQ ID NO 272
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                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
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                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/268,292 PRIOR FILING DATE: 2001-02-13
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; OTHER INFORMATION: Incyte ID No. US20030108871A1
US-09-919-039-318
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SEQ ID NO 318
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
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TYPE: PRT
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ENERAL INFORMATION:
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES ILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                 ThrAsnCysHisThrLysIleArgHisValAspAlaHisAlaThrLeuAsnAsp---Gly 89
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Query Match:
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
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LOCATION: (473)
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121 GlnThrPheValLeuAlaProGluGlySerValAlaAsnLysPheTyr---ValHisAsn
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                                                                              ValValValGlnValMetGlyLeuLeuSerAsnAsnAsnGlnAlaLeuArgArgPheMet 120
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US-09-763-902B-10 (1-830) x US-09-764-864-1044 (1-326)
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Best Local Similarity:
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GENERAL INFORMATION:
ADDITO:
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CURRENT FILING DATE: 2001-01-17
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US-09-814-777A-99
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Patent No. US20020142415A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: AU PQ6457 PRIOR FILING DATE: 2000-03-24
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APPLICANT: MUSCAT, George Eugene Orlando
TITLE OF INVENTION: NOVEL POLYPEPTIDES ANT
FILE REFERENCE: 21415-0003
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                                                              CAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTGAGGGGAACAAAC
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US-09-763-902B-10 (1-830) x US-09-907-495-2 (1-802) Oy 24 TCTCTTCAACCTTACTTCCCTGCAGCCCCTGGTTCCCCAAGGCAGAGG 71 ::: ::: :::	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: 10 Length: Matches: 64 Conservative: 27 Mismatches: 98 Query Match: 10 Gaps: 14	CURRENT APPLICATION NUMBER: US/09/907,495 CURRENT FILING DATE: 2001-07-16 PRIOR APPLICATION NUMBER: 60/218,383 PRIOR FILING DATE: 2000-07-14 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 802 TYPE: PRT ORGANISM: Homo sapiens US-09-907-495-2	US-09-907-495-2 ; Sequence 2, Application US/09907495 ; Patent No. US20020081696A1 ; GENERAL INFORMATION: ; APPLICANT: Meyers, Rachel ; TITLE OF INVENTION: 32529, A NOVEL HUMAN GUANINE NUCLEOTIDE EXCHANGE FACTOR ; TITLE OF INVENTION: FAMILY MEMBER AND USESE THEREOF ; FILE REFERENCE: MNI-175	429 LeuProGlyLeuHisPheSerThrCysSerPheSerCysSerValPheSerThrThrA 756 CTTTTCTATTTTTCTACTTGCCCA 779	::: 396	TCTTGTAGAGATATGCAAAACTCCGACTCTCAAGGATGTGAAGGAACACAAAGTTCATTTCTGT FroArgSerGlnCysCysPro	296 471 316 516 336 549
Alignment Scores: 6.68 Length: 1604 Pred. No.: 85.50 Matches: 64: Score: 85.50 Matches: 27 Percent Similarity: 35:00% Conservative: 27	PATOR FILING DATE: 1999-12-21 NUMBER OF SEQ ID NOS: 72 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 8 LENGTH: 1604 TYPE: PRT ORGANISM: Homo Sapiens US-09-746-91-8		564 AGCCCTAGCTCTGTÄGAGAAATGCAAACTCGACTCTCAAGGATGTGAGGAACACAAGTT	Qy 447 TCATCCTGACCGCCGAGGCCTCACCAGCAAGAGTGTGGAAGATCGCAAGTGACGCCTCT 506	354 ATGAAGCCACACCAAGCC :::::		Qy 72 AAATACCCTGGTGGAGCCCTCCTTCCATAGAACCAGAGATGGCATCTGTGGATTTCAAGA 131

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Best Local Similarity:
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                                                                                     PRIOR APPLICATION NUMBER: IL 133318 PRIOR FILING DATE: 1999-12-05 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                  TITLE OF INVENTION: PROTEOGLYCANS AND PHARMACEUTICAL COMPOSITIONS COMPRISING THEM FILE REFERENCE: 01/22063
CURRENT APPLICATION NUMBER: US/10/149,326
CURRENT FILING DATE: 2002-06-05
               SOFTWARE: PatentIn version 3.1 EQ ID NO 8
                                                                                                                                                                                                                                                                                                                                              equence 8, Application US/10149326
ublication No. US20030100492A1
ENERAL INFORMATION:
APPLICANT: Yayon, Avner
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                                                                                             APPLICANT: FOTSYth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for invention proliferation of E. col
FILE REFERENCE: ELITRA, 009A
CURRENT APPLICATION UNBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 458
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US-10-149-326-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 458, Application US/09741669 Patent No. US20020022718A1 GENERAL INFORMATION:
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ORGANISM: Escherichia coli
9-741-669-458
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US-10-273-680-2
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                                              FILE REFERENCE: MPIO1-317P1RNM
CURRENT APPLICATION NUMBER: US/10/273,680
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US 60/329,756
               PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                   APPLICANT: Millennium Pharmaceuticals, APPLICANT: Tomlinson, James E.
                                                                                                                  TITLE OF INVENTION: VELP2, A CONTILE OF INVENTION: SPECIFIC THEREFOR
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INVENTION: VELP2, A VASCULAR ENDOTHELIAL CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAAGATCGCAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGTGGCAG
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                                                                     TACTTGTTTGT
                                                                                                                                       TGTGCCGAGGTTGAACTCTTTTTTGTTGCTCAAGTTCTAGGAGTCCCTTTCCTGAATATA
                                                                                                                                                                        pHisMetLysHisPheCysCysLeuGluCys-GluThrValLeuGlyGlyGlnArgTyrI
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                                                                                                   leMetLysAspGlyArgProPheCysCysGlyCysPheGluSerLeuTyrAlaGluTyrC
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-982-610-24
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                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                          1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 1
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                                          1019 IleAlaLeuAlaArgGlyValArgSer
      201
                                                                              141 ATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGC
                                                                                                                                                                                                    90 CTCCTTCCATAGAACCAGAGATGGCATCTGTGGATTTCAAGA-
                                                                                                                                                                                                                                              33 CCTTACTTCCCTGCAGCCCCTGGTTCCCCAAGGCAGGGAAATACCCT---GGTGGAGCC
GGCGGCGTTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/446,648 FILING DATE: 1996-MAY-23 APPLICATION NUMBER: 08/22616 FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/982,610 FILING DATE: 17-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
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NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genentech)
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                                                                                              PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/870,133
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,649
                                                                                                                                                                               PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US 60/197,747
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/160,50:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Kapeller-Libermann, Ro
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/838,573
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN 39228, TITLE OF INVENTION: NOVEL HUMAN 39228, TITLE OF INVENTION: MOLECULES AND TOTAL PROPERTY. PROPERTY.
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Meyers, Rachel E.
                                                                                                                                                                                                                                                                                        TILE REFERENCE: MNI-250
                                   APPLICATION NUMBER: US 09/870,130 FILING DATE: 2001-05-29
                                                                              FILING DATE: 2000-05-26
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vo. US20030059919A1
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                  60/207,640
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88, 50566, AND 48118
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NUMBER: US 09/862,535 : 2001-05-21

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Query Match:
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SOFTWARE: FAS
SEQ ID NO 17
LENGTH: 725
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ORGANISM: Homo sapiens
S-10-160-501-17
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                                      476 HisProGluPheGluAlaGlyAsnValHisThrAspPheIleProGlnHisHisLysGln 495
                                                                                      401
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446 TTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCA------
                                                                                                                                                               341 CAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGA 400
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                                                                                 TCAGTGAAGTTTGAG----GGGAACAAACAACGGGACTTC-----
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                                                                                                                                                                                                        LeuArgTyrSerLeuArgGlnTyrAsnIleVal-----
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ThrProGlyHisProLeuLeuAlaProThrSerSerHisValProGlyLeuAsnSer 1280	Db 1261 ThrProGlyHi	_
TGGATAA	ОУ 189	
 oSerLeuSerSerSerGln	1241	
CCTGCAGAGCTGCTGAGGAGTTTGTCAATGTCTACTACACCA	Qy 147 CCTGCAGAGCT	
Ser 1240	Db 1239 Ala	
GCCCTCCTTCCATAGAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGG 146	Oy 87 GCCCTCCTTCC	_
CITCAACCTTACITCCTGCAGCCCCTGGTTCCCCAAGGCAGAAGAAATACCCTGGTGGA 86	Db 1221 LeuAlaProva	
	-09-763-902в	
46.7 Length: 2971 78.50 Matches: 55 32.178 Conservative: 19 23.918 Mismatches: 88 5.278 Indels: 68 9 Gaps: 7	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	
	; ORGANISM: Homo sapiens US-10-146-473-50	
version 3.0	: PatentIn	
UMBER: US 60/291,150 2001-05-15	PPLICATION N	
TION NUMBER US/10/146,473 DATE: 2002-05-15	CURRENT FILING DATE: 2002-	
ye Byeast Cancer Antigens	E OF INVENT	
Tseng		
Elisabeth		
Matthew	APPLICANT: Scanlan,	
0 Application US/10146473 to. US20030108888A1 WATION:	RESULT 15 US-10-146-473-50 US-10-146-673-50 ; Sequence 50, Applicatic ; Publication No. US20036 ; GENERAL INFORMATION:	
AsnLeuTyr 590	Db 585 ValLeuGly	
TTCTAGGAGTCCCTTTCCTGAATATATAC 721	Qy 692 GTTCTAGGAGT	
TyrAsnH1sAspGlySerTyrSerMetGlnIleGluAspLysThrPheGln 584	Db 568 TyrAsnHisAs	
GGTTG	Qy 638 CGGAGACACTC	
ThrArgAsnMetThrLeuLysAspGlyLysAsnAsnValAlaIleAlaValThr 567	Db 550ThrAi	
TGTGA	QY 578 AGAGAAATGCA	
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GACTGGGCCAGCTAGTGGGGGTGGCAGAGGTCTCTTTGCTTCATTCA	оу 518 састесссае	
	Db 516 IleLeuLysGl	
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1419	488 1399	428 1379	74 359	326 1339	320 1319	263 1299

earch completed: June 24, 2003, 19:42: ob time : 40.503 secs

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-MODEL-frame+ n2p.model -DEV-xlp
-Q-/cgn2_1/USFTO_spool/US09763902/runat_24062003_130341_12467/app_query.fasta_1.2254
-Q-/cgn2_1/USFTO_spool/US09763902/runat_24062003_130341_12467/app_query.fasta_1.2254
-DE-PIR_73 -QFMT=fastan -SUFFIX=PD.rpr -MINMATCH=0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS=blts -START=1 -END-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09763902_0CGN_1:_1_108_0runat_24062003_130341_12467 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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                                 287 GAGITITTTGAAATGITGCCTTCCAGCGAGTTCCAAATCAGCGTGGTA-----GACTGC 340
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 54 GluLysLeuSerSerLeuProPheGlnLysIleGlnHisSerIleThrAlaGlnAspHis 73
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                                                                 IleAspAlaSerCysLeuThrTrpGluGlyGlnGlnPheGlnGlyLysAlaAlaIleVal 53
                                                                                                ATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAATCCTTGAGT 286
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A;ACGESSION: CT A;ACJESSION TYPE: MRNA A;Residues: 1-127 <GRUD A;Cross-references: EMBL:X07315; NID:g35578; PIDN:CAA30278.1; PID:g35579 A;Cross-references: EMBL:X07315; NID:g35578; PIDN:CAA30278.1; PID:g35579 C;Accession: S00751
R;Grundmann, U.; Nerlich, C.; Rein, T.; Lottspeich, F.; Kuepper, H.A. Nucleic Acids Res. 16, 4721, 1988
Nucleic Acids Res. 16, 4721, 1980
A;Title: Isolation of cDNA coding for the placental protein 15 (PP15).
A;Reference number: S00751; MUID:88247772; PMID:3380696
A;Accession: S00751 C;Species: Homo sapiens (man) C;Date: 31-Dec-1988 #sequence_revision 0.000455 124.00 43.59% 26.50% 8.33% Length: Matches: Conservative: 31-Dec-1988 #text_change 24-Sep-1999 Mismatches: Indels: 127 31 20 54

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US-09-763-902B-10 (1-830) x H86248 (1-522)
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A;Gene: T23J18.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; & Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W., Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                 392 ATCTGTGGATCAGTGAAGTTTGAGGGG---AACAAACAACGGGACTTCAACCAGAACTTC
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                                                                                                                                                                  332 GTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTC
                                                                                                                                                                                                      380 AsnIleSerAsnLysLeuLysGlnLeuProPheAspGlnCysHisHisLeuIleSerThr 399
                                                                                                                                                                                                                                               278 TCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAA-----ATCAGCGTG
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                                       ValSerGlySerIleGlnLeuH1sGlyGluAspH1sProLeuArgPheSerGlnThrPhe
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                                                                                                                                                                                                                                                                                       SerLeuTyrAsnProThrSerLeuLeuThrPheGluGlyGlnThrIleTyrGlyValAsp
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s: GB:AE005172; NID:g6554189; PIDN:AAF16635.1; GSPDB:GN00141

    LysAsnIleAsnAspAlaTrpValCysThrAsnAspMetPheArg 120

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.S.; Maiti, R
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nuclear transport factor NTF2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YER009w
C;Species: Saccharomyces cerevisiae
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. a;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: B86405
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. Nansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
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A; Residues: 1-126 <STO>
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C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Haarer, B.K.; Corbett, A.; Kweon, Y.; Petzold, A.S.; Silver, enetics 144, 495-510, 1996
.;Title: SEC3 mutations are synthetically lethal with profilin ;Reference number: S72237; MUID:97044444; PMID:8889515
.;Accession: S72237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:U18778; NID:g603592; PIDN:A; Haarer, B.K.; Petzold, A.S.; Brown, S.S. ubmitted to the EMBL Data Library, July 1993 pescription: Identification of mutations that are Reference number: S41793; Accession: S41793
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Map position: 5R
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Residues: 1-125 <DIE>
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Residues: 1-84 <HAW>
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Residues: 1-84 <HAA>
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vion: S50467; S41793; S72237
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                                                                                                                                                                                                                                                                                                            GAMATGTTGCCTTCCAGCGAGTTCCAA-----ATCAGCGTGGTAGACTGCCAGCCTGTT 349
                                                                                                                                                                                                                                                                                                                                                SerMetLeuThrPheGluThrSerGlnLeuGlnGlyAlaLysAspIleValGluLysLeu 54
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                                                                                    GCCTCACCCAGCAACACAGTGTGGGAAGATCGCAAGTGACTGCTTCCGC
                                                                                                                        IleAspGluGluGlnAsnProGlnArg---PheSerGlnValPheHisLeuIle---
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                                                    -ProAspGlyAsnSerTyrTyrValPheAsnAspIlePheArg 120
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P.; Brown, S
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                                   hypothetical protein K08F4.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans. C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #teC;Accession: T23479
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C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000 C;Accession: T38039; T37728 C;Accession: T38039; T37728 Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, R;McDougall, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL109951; PIDN:CAB53052.1; A;Experimental source: strain 972h-; cosmid c1B9 R;Deylin, K.; Churcher, C.M.; Barreil, B.G.; Rajandr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
A: Introns: 3/1;
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A; Residues: 'SL',77-123
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A; Residues: 1-123 <MCD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-763-902B-10 (1-830) x T38039 (1-123)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt SerLeuTyrArgGluGluSerMetLeuSerPheGluGlyAlaGlnLeuGlnGlyThrLys}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAA-----ATCAGCGTG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt AlaThrGlnPheThrGlnPheTyrTyrGlnThrPheAspSerAspArgSerGlnLeuSer}
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                                                                                                                                                                                                                                                                                            ValThrGlyGluLeuLeuAspGluGluGlnMetAlaGlnArgTyrSerGlnValPhe
                                                                                                                                                                                                           ATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTC 508
                                                                                                                                                                                                                                                                                                                                                              ATCTGTGGATCAGTGAAGTTT---GAGGGGAACAACAACGGGACTTCAACCAGAACTTC 448
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L:268197;
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August 1999
                                                                                                                                                -AsnAsnAsnGlyAsnTyrTyrValLeuAsnAspLeuPhe 118

    fission yeast (Schizosaccharomyces pombe)

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Matches:
Conservative:
Mismatches:
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 81.6-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X; Liu, Z.A.; Luros, J.S.; Maiti, F. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis. A;Recession: H86398
                                                                                                                                                                                                                                                                             protein F17L21.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from Molecule type: DNA Residues: 1-537 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL: Z68879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 LysIleGlnSerIleLysGlyTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 CGGCGTTTGCTGTCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                             GACTGCTTCCGCTTCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GinSerPheLeuLeuGlyGlnGlnGlyGlnLysLys:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt AlaAlaGluGlnValGlyGlyAlaPheCysHisGlnPheTyrIleThrValSerGluAsn}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99/1; 140/3; 161/3;
                       GB:AE005172;
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23.62%
7.12%
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                NID: 99802547; PIDN: AAF99749.1;
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                                                                                                                                                                                                                             Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                              520
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Conservative:
Mismatches:
Indels;
Gaps:
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             GSPDB: GN00141
                                                                                                                                                                                                                                              S.; White, O.;
                                                                                                                                                             Khaykin, E.;
Maiti, R.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499
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                                                                                                                                                                                                                               Dewar,
                                                                                                                                                           Marziali
                                                                                                                                Tallon,
                                                                                                                                                                                                                            Alonso,
                                                                                                                                                                                Xim,
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                                                                                                                                                    A; Map position: 1
A; Introns: 33/1; 63/3;
C; Superfamily: yeast n
US-09-763-902B-10.(1-830) x T23921
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                    A; Experimental source: clone R05D11
                                                                                                                                                                                                                                             A;Cross-references: EMBL:275546; PIDN:CAA99890.1; GSPDB:GN00019; CESP:R05D11.3
                                                                                                                                                                                                       A; Gene: CESP:R05D11.3
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Best Local Similarity:
Query Match:
DB:
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A;Map position: 1
C;Superfamily: yeast
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                                                                                                                                                                                                                                                                                          Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 ATCTGTGGATCAGTGAAGTTTGAGGGGAACAAACAACGG---GACTTCAACCAGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 GTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACACGGTCCTTGTTGTC :::|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 TCCTTGAGTGAGTTTTTTGAAATGTTGCCT-----TCCAGCGAGTTCCAAATCAGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGGCGTTTGCTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ValSerGlyAsnLeuGlnLeuAlaGlyGluGlnHisAlaLeuLysPheSerGlnMetPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 CGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAA
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                                                                                                                                                 3; 96/3
nuclear transport
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                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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Gaps:
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500

186

440

171

Accession:

;Molecule type: DNA ;Residues: 1-122 <STO> ;Cross-references: GB;

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96

Percent Similarity:
Best Local Similarity:
Query Match:

Alignment Scores:

A; Introns: 66/3; A; Map position: Gene: CESP:K08F4.2

Experimental source:

Accession: T23479

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                               US-09-763-902B-10 (1-830) x T40805 (1-434)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: SPDB:SPBP8B7.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:AL032684;
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GlnGlnGluIleHisAsnLysIleLeuAspLeuAspPheGlnAsnCysLysValLeuIle 81
                                                                             ThrLysLysSerThrLeuIleHisGlyAspGluGlyGluSerIleSerLeuCysHisGly
                                                                                                                    ATGGGCACAGCCACCCTGGTCTGG-----AATGGCAATGCTGTTTCAGGACAAGAATCC
                                                                                                                                                                                            TTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTAC
                                          TTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGC
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91.50
42.37%
27.12%
6.15%
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Library, October 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAA21796.1; -; clone p1 p8B7
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suppressor 2 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: G1-to-S transition protein; protein C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 66, 45-54, 1988
A; Title: Nucleotide sequence of the SUP2(SUP35) gene of Saccharomyces cerevisiae
A; Reference number: JT0323; MUID:88329727; PMID:3047009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: A yeast gene required for the G1-to-S transition A;Reference number: S00488; MUID:88296422; PMID:2841115 A;Accession: S00488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S00733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: SUF12 suppressor protein of yeast. A; Reference number: S00733; MUID:88172503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Wilson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kushnirov, V.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-52,'C',54-685 <KIK>
A;Cross-references: GB:Y00829; EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z46727; NID:g1289283; PIDN:CAA86677.1; R;Kikuchi, Y.; Shimatake, H.; Kikuchi, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S49764
A;Accession: S49768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Murphy, L.; Harris, D.E. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-685 <KUS>
                             Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:SUP35; SUF12; GST1; SUP2; MIPS:YDR172w
A;Cross-references: SGD:S0002579; MIPS:YDR172w
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                                                Percent Similarity:
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:Kushnirov, V.V.; Ter-Avanesyan, M.D.; Telckov, M.V.; Surguchov, A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: JT03
                                                                                                                                                                                                                                                                         ;1-123/Domain: A <DOM1>
;42-119/Region: 10-residue repeats
                                                                                                                                                                                                                                                                                                            Superfamily: suppressor 2 protein; translation elongation; Reywords: duplication; GTP binding; nucleotide binding; P.
                                                                                                                                                               406-409/Region: GTP-binding
                                                                                                                                                                                                                     159-222/Region: glutamic acid/lysine-rich 254-685/Domain: C CDOM4>
                                                                                                                                                                                                                                                        124-253/Domain: charged <DOM2>
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800733; JT0323; 849768; 800488; A26742; 800533; 805723
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                                                                                                                                               GTP (Lys)
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                                 Conservative: Mismatches:
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US-09-763-902B-10 (1-830) x B72468 (1-353)
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Best Local Similarity:
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                                                                                                                                                                                                                                                          C; Superfamily: Aeropyrum pernix hypothetical protein
                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-353 <KAW>
A;Cross-references: DDBJ.AP000064; NID:g5105945; PIDN:BAA81402.1;
A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein APE2387 - Aeropyrum pernix (strain K1) ,
C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C.Accession: B72468
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                                                                                                                                                                                                                                                                                 Gene: APE2387
                                                                                                                                                                                                                                                                                                                                                                                   Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawarabayasi,
                                                                                                                                                                                                                                                                                                                                                                                                                           H.; Takamiya, M.; Masuda,
Res. 6, 83-101, 1999
                             213
                                            243 GluLeuLeuProAlaIleArgHisGlyAlaProProProGlnLeuProMetThrThrThr
                                                                                                                                                                                                                                                                                                                                                                       preliminary
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                          TGTCCCGCCTGT-
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                -ACATGGGCACAGCCACCCTGGTCTGGAATGGCA 257
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i, T.; Tanaka,
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T.; Kudoh, Y.;
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Best Local Similarity:
Query Match:
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A; Introns: 292/3;
                                                                                                                                                                                                                                                                                                                                                                                   Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F7K15.80 - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: ATSP: F7K15.80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T49237
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Residues: 1-485 <OBE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                      No.:
405
             204 ePheCysArgAsnCysSerLysGlyArgCysLeuMetProSerArgPheArgGluArgAs
                                                        454
                                                                                      188
                                                                                                                                 168 GluProProGluTrpLeuProAspSerLeuAlaSerThrCysMetGlnCysSerThrPro 187
                                                                                                                                                                                           148 ProProLeuLeuGluProSerGlyIleAsnTyrSerValTyrLysGluLeuLeuGluAla 167
                                                                                                                                                                                                                        Scores:
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                                              CAGGATGAAGTTCTGGTTGAAGTCCCGTTGTTTGTTCCCCTCAAACTTC-
                                                                        PheThrAlaIleThrCysGlyArgHisHisCysArgPheCysGly------Gly-Il
                                                                                                                                                               AAGAGACCT-----CTGCCACCCCCACTAGCTGGCCCAGTCCTGGAAGCGGAA-----
                                                                                                     -----GCAGTCACTTGCGATCTTCCACACTGT---GTTGCTGGGTGAGGCCTGGGCGGT 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCTGTTTCAGGACAAGAATCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGT 317
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Matches:
Conservative:
Mismatches:
Indels:
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53
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                224
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Db 988 ProSerGlnArgSer	tive es: SerT	RESULT 13 T90078 probable RNA-directed DNA polymerase (EC 2.7.7.49) - Chlorella vulgaris retrotransposon probable RNA-directed DNA polymerase (EC 2.7.7.49) - Chlorella vulgaris retrotransposon R;Alternate names: reverse transcriptase C;Species: Chlorella vulgaris C;Species: Chlorella vulgaris C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000 C;Accession: T00078 R;Higashiyama, T:: Noutoshi, Y:; Fujie, M.; Yamada, T. EMBO J. 16, 3715-3723, 1997 A;Title: Zepp; a LINE-like retrotransposon accumulated in the Chlorella telomeric region A;Reference number: Z14092; MUID:97361851; PMID:9218812 A;Accession: T00078 A;Cession: T00078 A;Cession: T00078 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: J-1309 <hig>A;Cross-references: EMBL:AB008896; NID:g3063386; PIDN:BAA25763.1; PID:g3073779 A;Experimental source: strain C-169 C;Genetics: A;Map position: 5 A;Map position: 5 A;Map position: 5 A;Map position: retrotransposon Zepp C;Keywords: nucleotidyltransferase</hig>	Db 224 nProGlnArgValCysAspSerCysTyrGluArgLeuAspProLeuGlnCysValLeuI1 244 Qy 396
A; Molecule type: DNA A; Residues: 1-328 <whi> A; Residues: 1-328 <whi> A; Cross-references: GB: AE002091; GB: AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; GB: AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; GB: AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 964 A; Cross-references: GB: AE002091; AE000513; NID: 96460446; PIDN: AAF12158.1; PID: 96400513; NID: 964000513; NID: 96400513; NID: 96400513; NID: 96400513; NID: 96400513; NI</whi></whi>		1148 189 1168 1188 1188 1198 1208 1208 1227 44	Db 1065 AlaArgProGlyAlaSerGlySerAspGly

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Pred. No.:
                                                                                                         A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
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I38346
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                                                                                                                                                                                                                                    lastic titin - human (fragment); Species: Homo sapiens (man)
;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000; Accession: I38346
;Labeit, S.; Kolmerer, B.
cience 270, 293-296, 1995
;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity. Reference number: A57430; MUID:96026330; PMID:7569978
;Accession: I38346
;Status: preliminary: translated from GB/EMBL/DDBJ
;Molecule type: mRNA
;Residues: 1-7962 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 snArgTyrLeuArgSer 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCCACCAGGGT----ATTTCCTCTGCCTTGGGGAACCAGGGGCTGCAGGGAAGTA- 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCTGATCCACATAGGTCTTGAAATCCACAGATGCCATCTCTGGTTCTATGGAAGGAGG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspProAlaLeuAlaAlaAlaValGlnThrAlaLeuMetSerProSerLeuArgValTyr 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- AGGTTGAAGAGAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLeuHisLeuGlyAspAsnAlaLysAlaThrLeu-LeuThrArgGlyLeuArgGluMetA 218
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     5.67
86.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ArgGluLeuGlyValValLeuCysAlaLysGlyLeuAlaProAspGly 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValLeuLysAsnValIleAlaValAlaAlaGlyMetGlyAspGl 198
  Length:
Matches:
7962
62
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Qy Db	OV DO V	Db Qy	Оу [*]	Qy Db	Qy	Öγ	Qy Db	Qy Db	Qy Db	Qy	Qy Db	Db.	Percent Best Lo Query M DB: US-09-7
	294 2816 sLysAla 241 ggTggCC	340 GCAGTC	400 TCCACAC	436 2781 AspThr	481 TGTGTT	535 2750 LeuGlui	553 AAGAGA 2730 GlyArg	604 CTTGAG 2711 LeuAsn	664 GGCACA	715 ATTCAG- 2680 IleSerV	775 CAAGTA 2661 SerVal	826 TGTATT 2641 CysThr	Similarity cal Similar atch: 63-902B-10
gGlnLeuProProSerPheAla/	-AAAAACTCACTCAAGO ::: ::: aGluAsnSerIleGly:	GCAGTCTACCACGCTGATTTGGAACTCGCTGGAAGGCAACATTTCAAlaThrieuVaiPheAsniysVaiAsnileAsnaspSerG	SATGACAACAAGGACC	LysLeuArgProThrP	GTGTTGCTGGGTGAGGCCTGGGCGGTCAGGATGAAGTTCTGGTT-	CACTAGCTGGCCCAGTCCTGGAAGCGGAAGCAGTCACTTGCGATC	AAGAGACCTCTG GlyArgAspValCysGlyAlaL	CTTGAGAGTCGAG euAsnSerThrLysArgAspA	GGCACAGTGGAGTCTGCAGTGT	GAAAGGGAC 	GAAAAATAGAAAAGTT . stantagaaaaagtT	TGTATTATTAAATTATTGTCAGAATTTCCAGAATC- 	36.00% 22.55% 5.78% 2
	BATTCTTGTCCTGAAAC; ::: [hrAlaSerSerLysThi	AACTCGCTGGAAGGC ::: AsnLysValAsnIle	STGGTCTGGCTTGGT	GAAGTCCCGTTGT roGluTyr-ArgThr	GCGGTCAGGATGAAGTT 	TCCTGGAAGCGGAAG 	euValSerThrLeuG	GTTTGCATTTCTCTA ::: laGlyGlnTyrSerC	CTCCGCAACAACAGA	ACTCCTAGAACTTGAGC ::::: spGlyPheAsnIleThr	AAAGTTTACTACTTTGAAAAG ::::: ysSerIleIleLeuGluS	GÄATTTCCAGAATC- :: ysGluProAlaAlap	Conservative: Mismatches: Indels: Gaps: (1-7962)
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r 2856		- 295 y 2816	G 341 - 2798	A 401 - 2798	- 437 Y 2780	C 482 - 2766	- 536 u 2749	A 554 a 2729	C 605 e 2710	C 665 e 2699	T 716 o 2679	G 776 s 2660	

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Command line parameters:

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-MODEL-framet_12p.model -DEV-xlp
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-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDE-10 -XGAPDEXT-0.5 -FGAPDP-6
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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NTF2_YEAST
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                 RX MEDLINE=21638749; PubMed=11780052;

RA DeLoukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA DeLoukas P., Matthews L.H., Ashurst J.P., Babbage A.K., Bagguley C.L.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Beasley O.P., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hunkle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kinberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.G., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND FUNCTION.
MEDLLINE-20036817; PubMed-10567585;
Black B.E., Levesque L., Holaska J.M
"Identification of an NTF2-related f
regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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C114_MOUSE
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YNBT_YEAST
CORI_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guzik B.W., Levesque L., Prasad S., Bor Y.C Paschal B.M., Rekosh D., Hammarskjold M.L., "NXTI (pl5) is a crucial ceilular cofactor intron-containing RNA in mammalian cells."; Mol. Cell. Biol. 21:2545-2554(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as lon modified and this statement is not remove entitles requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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Dssareh-Nazari B., Maison C., Blac
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                                                                                                                      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20036817; PubMed-10567585;
Black B.E., Levesque L., Holaska J.
"Identification of an NTF2-related
regulates nuclear protein export.";
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; (MEDLINE=21085660;
                                        Nature 409:685-690(2001).
                                                                                                             Wynshaw-Boris
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                                                                         "Functional annotation
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tRNA, and
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Eutheria; Rodentia;
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/6J; TISSUE-Embryo;
5660; PubMed-11217851;
shibata K.
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Stimulator of protein Also plays a role in tmRNA (By similarity).
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                                                                                                           Yoshida
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protein 1.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                           Q9NPJ8; Q9H8U0;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
15-JUN-2002 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity: y Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transport; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                     NTF2-related
                                                                    NXT2_HUMAN
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SUBCELLULAR
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  sapiens (Human)
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dexport protein 2 (p15-2 protein)
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BAB22670.1;
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358EAFDC19FE4594
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Matches:
Conservative:
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Indels:
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  Kang Y.,
"p15-2, a
                                             EMBL;
EMBL;
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EMBL;
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Isogai T., Ota T., Hayashi K.,
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Submitted
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    Pfam; PF02136; NTF7:
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                                                                                                                                                                                                                                                                                                                           Zhao M., Song H., Li N., "A novel gene expressed i Submitted (DEC-1999) to t
                                                                                                                                                                                                                                                                                                                                                        TISSUE-Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol.
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                                                                                   AJ277591; CAB96371.1;
AJ278323; CAC01129.1;
AF246127; AAF78034.1;
                                              AL031387;
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l genes expressed !
tted (NOV-1999) to
                                     AL031387;
                                                                            AF201942;
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(MAR-2000)
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                                    ; AAF87325.1;
; CAB41301.1;
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NTF2_DOMAIN;
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Ninomiya K., Iwayanagi T., "NEDO human cDNA sequencing project.";
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A. (ISOFORM
                                                                                                      the cytoplasm.
ALTERNATIVE PRODUCTS: 2 isoforms; A produced by alternative splicing.
SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NXF1) belongs to a multigene family of pors with a conserved modular architecture Cell. Biol. 23:8996-9008(2000).
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1 N., Gu W., Han 7

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                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20036817; PubMed-10567585;
MEDLINE-20036817; PubMed-10567585;
MEDLINE-20036817; Pidlaska J.M., Woo
"Identification of an NTF2-related factor
regulates nuclear protein export.";
"Onll Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Alternative
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STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.
George R.A., Lewis S.E., Richards S., Ashburner M
                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brack
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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16-OCT-2001
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(Rel. 41, Last annotation update)
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ATSL > VTNHVPALCTAGRGPTFAARPAGPTPSLVSSR
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         R.A.,
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         , Gocayne J.D.,
R.A., Galle R.F
M., Henderson S
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122

GATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTTGTCAATGTCTAC

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Alignment
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Query Match:
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.; Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.; Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.; Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merson D.R., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menson D.R., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou X., Zhu X., Smith H.O.,
RA Zheng S.H., Wopers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000)
  US-09-763-902B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Talali M., Kalush F., Karren G. H., Kernigon J.A., Kerchum I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sutton G.G., Wortman J.R., Y
Brandon R.C., Rogers Y.-H.C.
Wan K.H., Doyle C., Baxter E
Wan I.H., Agbayani A., An
Abril J.F., Agbayani A., An
                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0028411; Nxt1.
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                                                                                                                                                                                                                                                                          PROSITE; PS50177; NTF2_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Stimulator of protein export for proteins. Also plays a role in the nuclear tRNA, and mRNA (By similarity).
SUBUNIT: Preferentially binds Ran-GTP (By s
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rs Y.-H.C., Bla
, Baxter E.G.,
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C., Blazej R.G., Champe N
E.G., Helt G., Nelson C.
                                                                                                                                                                                                                              ; mRNA transport; Nuclear NTF2.
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Conservative:
Mismatches:
Indels:
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Baldwin D.,
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                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                  Bradshaw-Cordum H., Scott K., Graves T.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Stimulator of protein export for NES-contaproteins. Also plays a role in the nuclear export of tRNA, and mRNA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _CAEEL
                                                                       EMBL; AF156960; AAD54945.1;
EMBL; AC024852; AAK66028.1;
HSSP; P13662; 10UN.
                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Black B.E., Levesque L., Holaska J.M., Woc
"Identification of an NTF2-related factor
regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NXT1_CAEEL Q9U757;
                                                                                                                                                       or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
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                                           WormPep;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20036817; PubMed=10567585;
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                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                SUBUNIT: Preferentially binds Ran-GTP (By simi SUBCELLULAR LOCATION: Nuclear (By similarity).
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                        P13662; 10UN.
ep; Y71F9AM.5; CE26780
ep; Y71F9AM.5; NTF2.
epro; IPR002075; NTF2.
epr02136; NTF2; 1.
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hat binds Ran-GTP an
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Best Local Similarity:
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interacts wi
J. Cell Biol
[3]
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DOMAIN
SEQUENCE
                                                                                                                                                                Grundmann U.,
"Isolation of
Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTF2_HUMAN P13662;
 Paschal B.M., Gerace L.,
Paschal B.M., Gerace L.,
"Identification of NTF2, a cytosolic factor for
interacts with nuclear pore complex protein p62.
" Cell Biol. 129:925-937(1995).
                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                          MEDLINE-95263674;
                                                                                                           SPECIES-Human
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse),
                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear transport
NTF2 OR PP15.
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15-JUN-2002
                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                        SPECIES-Human
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606, 10090,
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human),
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                                                                                                                                                                                                                   MEDLINE-88247772; PubMed-3380696;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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19
137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 1)
                                                                                                                                                             Nerlich C., Rein T., Lottspeich cDNA coding for the placental pures. 16:4721-4721(1988).
                                                                                                                            N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                       PubMed=7744965;
                                                                                                                                                                                                                                                                                                                                                                                                                   13, Last sequence update)
41, Last annotation update)
factor 2 (NTF-2) (Placental
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Catarrhini;
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Conservative:
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per H.A.; (PP15).";

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Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y. Konno H., Kouda M., Koya S., Kulhara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shinata K., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yanamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu W., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Rat; TISSUE-nature, Bullock T.L., Sterman, Kent H.M., Clarkson W.D., Clar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanagaki T., Carninci P., Fukuda S., Akimura I
Hanagaki T., Hara A., Hayatsu N., Hiramoto
Imotani K., Ishii Y., Itoh M., Tanua
Konno H., Konda Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98202576; PubMed-9533885; Stewart M., Kent H.M., MCCoy A.J.; Stewart M., Kent H.M., MCCoy A.J.; "Structural basis for molecular recognition between nuclear transport factor 2 (NTF2) and the GDP-bound form of the Ras-family GTPase
EMBL;
                                                                         EMBL;
EMBL;
                                                                                                                                                                         use by non-profit institutions as long as its modified and this statement is not removed. Usage entities requires a license agreement (See http:/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nuclear protein import is decreased by transport factor 2 (NTF2) that do not b. J. Mol. Biol. 272:716-730(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96300274;
Bullock T.L., Clar
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                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.
INTERACTS WITH THE NUCLEOPORIN P62 AND WITH RAN. ACTS AT A
RELATIVELY LATE STAGE OF NUCLEAR PROTEIN IMPORT, SUBSEQUENT TO
INITIAL DOCKING OF NUCLEAR IMPORT LIGAND AT THE NUCLEAR ENVELOY
COULD BE PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS 1
ASSEMBLE AT THE PORE COMPLEX DURING NUCLEAR IMPORT.
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                                                                                              X07315;
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                                                 BC003955; AAH03955.1; BC002348; AAH02348.1;
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D., Bullock T.L.,
GenBan
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S., Fukunishi Y., Furun
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Pur.T., Shelsta H.N., Dasso M.;
"Identification of a pl0(NYF2) homologue in Xenopus.";
"Identification of a pl0(NYF2) homologue in Xenopus.";
"Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS.
-INTERACTS WITH THE NUCLEOPORIN P62 AND WITH RAN. ACTS AT A
RELATIVELY LATE STAGE OF NUCLEAR PROTEIN IMPORT; SUBSEQUENT TO TH
INITIAL DOCKING OF NUCLEAR IMPORT LIGAND AT THE NUCLEAR ENVELOPE.
                                                                                                                                Aenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Cranlata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                            NTF2_XENLA
042242;
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                                                                                                                      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                              SEQUENCE FROM N.A.
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15-JUL-1999 (Rel.
16-OCT-2001 (Rel.
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PF02136; NTF2; 1.
TE; PS50177; NTF2_DOMAIN;
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esobatrachia; Pipoidea; Pipidae;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.lsb-
or send an email to license@isb-sib.ch).
     SEQUENCE FROM N.A. STRAIN-ATCC 26555;
                                                         Eukaryota; Fungi;
Saccharomycetales;
NCBI_TaxID-5476;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                 Candida albicans (Yeast).
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SEQUENCE 127 AA; 14477 MW;
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                                                                          Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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US-09-763-902B-10 (1-830) x NTF2_CANAL (1-124)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence of Candida albicans and Yarrowia lipolytica homolog Saccharomyces cerevisiae NTF2 gene.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
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                                                                                                                                                                                                            GTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCACA
                                        GAAATGTTGCCTTCCAGCGAG-----TTCCAAATCAGCGTGGTAGACTGCCAGCCTGTT
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Lounn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

And Chung M.K., Conn L., Conway A.B., Fansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Kim X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Alin X., Feterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Saland H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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NTF2 OR AT1G27970 OR F13K9.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50177; NTF2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce,
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                                                    GlyLeuTyrGlnGluAlaSerMetLeuThrPheGluGlyGlnLysIleGlnGlyValGln
                                                                                                              CGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAA
                                                                                                                                                                                                                                      GCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCC
TCCTTGAGTGAGTTTTTTGAAATGTTGCCT--'--
                                                                                                                                                                         SerLysAlaPheValGluHisTyrTyrSerThrPheAspThrAsnArgValGlyLeuAla
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Conservative:
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NTF2_YEAST
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16-OCT-2001 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Nuclear transport factor 2 (NTF-2) (NU
NTF2 OR YEROODW.
Saccharce...
       This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTF2_YEAST P33331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mosedale D., Nakahara K., Namath A., Norgren R., Oefner F
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aviles E., Berno A., Brennan T., Carpenter J., Cher Chung E., Duncan M., Guzman E., Hartzell G., Hunicl Hyman R., Kayser A., Komp C., Lashkari D., Lev H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288c / AB972;
Dietrich F.S., Mulligan J.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-84 FROM N.A. Haarer B.K., Petzold A.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96178681; PubMed=8600522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                   Role of the nuclear transport factor p10 in nuclear import."; science 272:120-122(1996).
                                                                                                                                                                                                        EUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE N
INTERACTS WITH VARIOUS NUCLEOPORINS AND WITH RAN-G
PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTOR
AT THE PORE COMPLEX DURING NUCLEAR IMPORT. IN VITE
GDP ASSOCIATION, IN THE PRESENCE OF GTP, TRIGGERS
THE KARYOPHERIN ALPHA-BETA COMPLEX, ALLOWING NUCLE
                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: CONTAINS 1 NTF2 DOMAIN
                                                                                                                                                                                         OF KARYOPHERIN ALPHA AND THE NLS SUBSTRATE.
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(JUL-1993)
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e EMBL/GenBank/DDBJ
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Carpenter J., Chen E., Che
Hartzell G., Hunicke-Smith
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                                                                                                                                                                                                                                                                                  THE NUCLEUS.
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                                                                               restrictions
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Cherry J.M.
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EMBL; U18778; AAB64542.1; EMBL; L22204; AAB49379.1;

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Best Local Similarity:
Query Match:
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RRAP RTT ARREST
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Q9UN86; O75149; O60600; Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
E Ras-GTPase-activating protein binding protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport; Protein transport.
DOMAIN 8 121
                                              "unaracterisation and chromosomal location of G3BP-1 and G3BP-2a/b, members of a novel SH3 domain-binding and RNA-binding protein family implicated in signal transduction."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
             SEQUENCE FROM N.A. TISSUE-Brain;
                                                                                                                     ISSUE-Brain;
                                                                                                            ennedy D., Mattick J.S.;
                                                                                                                                    EQUENCE FROM N.A.
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S0000811; NTF2
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PubMed=9734811;
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                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
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Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prigent M., Barlat I., Langen H., Dargemont C.;
"IkappaBalpha and IkappaBalpha /NF-kappa B complexes are
the cytoplasm through interaction with a novel partner, F
                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kennedy D., Ru K., Mattick J. Submitted (MAR-1998) to the I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3-binding protein
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Kotani H., Nomura
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AF051311;
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PS50102; RRM; 1.
PS00030; RRM_RNP_
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                                                                                                                                                                                         IPR002075;
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PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED
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 Percent Similarity:
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/ Match:
                       -1- FUNCTION: PROBABLE SCAFFOLD PROTEIN
TRANSPORT (POTENTIAL)
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A
PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                   Kennedy D., Mattick J.S.; "Characterisation and G3BP-2a/b, "Characterisation and chromosomal location of G3BP-1 and G3BP-2a/b, members of a novel SH3 domain-binding and RNA-binding protein family
                                                                                                                                                                                         binding protein and structural confirmation that these contain an RNA recognition motif.", Biomed. Pept. Proteins Nucleic Acids 2:93-99(1997).
                                                                                              implicated in signal transduction.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                            Kennedy D., Wood S.A., Ramsdale T., Mattick J.S.;
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ras-GTPase-activating protein binding protein
binding protein 2) (G3BP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                  P97379; Q9R1B8;
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MEDLINE-98236259; PubMed-9575347;
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               · ! - SIMILARITY; CONTAINS 1 RNA RECOGNITION MOTIF (RRM)
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AspMetPheArgTyrGluAsp 135
                                                                                                        CAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGT
                                                                                                                                           ValValValGlnValMetGlyLeuLeuSerAsnSerGlyGlnProGluArgLysPheMet 109
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IPR000504; RNA_rec_mot.
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MISSING (IN ISOPORM B).

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FWLWNTOPF (IN REF. 1).

FB8BC2086123A5CE CRC64;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Protein transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-cv. Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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                        ATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTC
                                                                            ATCTGTGGATCAGTGAAGTTTGAGGGGAACAACAA---CGGGACTTCAACCAGAACTTC
                                                                                                             ValAspCysGlnPro
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                                                                                                                                                               AlaIleAlaGlyLysLeuGlySerLeuProPheAlaGlnCysHisHisAspIleAsnThr
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                                                   ValSerGlySerLeuArgThrGlyProAspGluH1sProLeuLysPheSerGlnMetPhe
                                                                                                                                                                                                                        SerLeuTyrGlnAspGlySerMetLeuThrPheGluGlyGlnGlnPheLeuGlyAlaAla
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Last annotation update)
tor 2 (NTF-2):
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84100EBB62AB1BD1 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.

Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Dominguez A., Revuelta J.L., Moreno S., Armströng J., Forsburg S.L.,

Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

Nature 415:871-880(2002).

-1- FUNCTION: FACILITATES PROTEIN TRANSPORT INTO THE NUCLEUS. COULD BI
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01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Probable nuclear transport factor 2 ()
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Holroyd
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EMBL; Z68197; CAA92380.2; -
HSSP; P13662; 1A2K.
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                                   Transport;
                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Wood V., Gwilliam R., Rajandream M
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PART OF A MULTICOMPONENT SYSTEM OF CYTOSOLIC FACTORS THAT
AT THE PORE COMPLEX DURING NUCLEAR IMPORT (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: CYTOPLASMIC (By Similarity).
-1- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
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                                                                   PF02136; NTF2; 1.
TE; PS50177; NTF2_DOMAIN; 1.
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SEQUENCE

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 Alignment Scores:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ras-GTPase-activating protein binding protein 1
binding protein 1) (G3BP-1).
G3BP OR G3BP1.
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                                                                                                               Strausberg R. Submitted (AI
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Debussche L., Dugue A., Schweighoffer F.,
                                                                                                                                                                                                                                         TISSUE-Placenta;
MEDLINE-96220439; PubMed-8649363;
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                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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                                                                                                                                                                             Ras-GTPase-activating protein SH3-domain-binding Cell Biol 16:2561-2569(1996)
SUBCELLULAR LOCATION: Cytoplasmic (Probable)
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF
                                                                              HALLEG (APR-2001) to the EMBL/GenBank/DDBJ FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT NTRANSPORT (POTENTIAL).
                                                                      SUBUNIT: BINDS TO THE SH3 DOMAIN OF
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InterPro; IPR000504;
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                                                                                            90 ValValValGlnValMetGlyLeuLeuSerAsnAsnAsnGlnAlaLeuArgArgPheMet
                                                                                                                                           71 ThrAsnCysHisThrLysIleArgHisValAspAlaHisAlaThrLeuAsnAsp --- Gly
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Search completed: June 24, 2003, 19:32:09 Job time: 16.6012 secs

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NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10
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-0=-/cgn2_1/USPTO_spool/US09763902/runat_24062003_130341_12453/app_query.fasta_1.2254
-D0=-SPTREMBL_21 -QFMT=-fastan -SUFFIX=-02F.rspt -MATRIX=D0-1.1 -LOOPEL=-0
-0.00PEXT=0 -UNITS-5HS -START=1 -EUD=-1.-MATRIX=blosum62 -TRANS-human40.cdi
-USTS-45 -DCCALICN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
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ALIGNMENTS

RESULT	17					
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AC	Q8T2G7;					
DŢ	01-JUN-2002	(TrEMBLrel. 21, Created)	1, Created)		*	
DŢ	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)	l, Last seq	uence updato	е)	
Ŋ	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)	l, Last ann	otation upda	ate)	
DE	Hypothetica:	Hypothetical 19.0 kDa protein.	tein.			
S	Dictyosteli	Dictyostelium discoideum (Slime mold).	(Slime mold	•		
గ	Eukaryota; 1	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.	tyosteliida:	; Dictyoste	lium.	
0X	NCBI_TaxID=44689;	14689;			-	
RN	Ξ					
RP	SEQUENCE FROM N.A.	OM N.A.		•		
R	STRAIN-AX4;		•			
₽ ·	Gloeckner G	., Eichinger L	, Szafrans	ki K., Pach	Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,	
RA	Lehmann R.,	Baumgart C.,	Parra G., A	pril J.F., (Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,	
RA	Tunggal B.,	Cox E., Quail	M.A., Plat	zer M., Rose	Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;	
RT	"Sequence a	"Sequence and Analysis of Chromosome 2 of Dictyostelium.";	Chromosome	2 of Dicty	ostelium.";	
RL	Submitted (1	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases	he EMBL/Gen	Bank/DDBJ da	atabases.	
DR	EMBL; AC115	EMBL; AC115607; AAL92371.1; ~.	1, -			
X	Hypothetical protein.	l protein.				
SQ	SEQUENCE	167 AA; 19039 MW; E16E4A5F4DA00BAA CRC64;	MW; E16E4.	A5F4DA00BAA	CRC64;	
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                                                                                   Pred. No.:
                                                                                               Alignment Scores:
                                                                                                                               O'Neil S., Harris D., Wood V., Rajandream M.A., Barrell B.G., Submitted (JAN-201) to the EMBL/GenBank/DDBJ databases. EMBL, AL512562; CAC21476.1; -. InterPro; IPR002075; NTF2. pfam, PF02136; NTF2; 1.
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01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                     Eukaryota; Fung1; Ascomycota;
Schizosaccharomycetales; Schiz
                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                        SPAPBIA10.03
                                                                                                                                                                                                                                                                                                   Putative nuclear export factor.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=4896;
                                                                                                                                                                                                                                            Schizosaccharomyces
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                                                                                                                                                                                            972H-;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGAAGATCGCAAGTGACTGCTTC
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45.39%
29.08%
10.44%
                       1.96e-06
142.00
52.89%
25.62%
9.54%
                                                                                                                       23029 MW;
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Conservative:
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. INFPONBARE;
SASAK1 T., MATSUMOTO T., 1
"OTYZA SALLYA (Japonica cu
clone:P0415A04.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar group).
Eukaryota; Viridiplantae; Etreptophyta; Et
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003345; BAB90110.1; -... 496BE9A02E1E9670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P0415A04.24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                               Scores:
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Lys 110
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                                                                                           CTACACCACCATGGATAAGCGGCGCGTTTGCTGTCCCGCCTGTACATGGGCACAGCCAC
                                                                                                                                GlyTrpSerAspGlnCys-AspValValAlaArgAla-----PheValGluTyrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HisValPheSerTyrArg------SerAlaThrThrGlnProAspAspThrIlePhe
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                                                        {\tt rTyrGlnThrPheAspThrAsnArgAlaAlaLeuAlaAlaLeuTyrGlyGlnThrSerMe}
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Last annotation updat
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tunggal B., Cox E., Quail M.A., Platzer Sequence and Analysis of Chromosome 2 o submitted (APR-2002) to the EMBL/GenBank, EMBL, AC115613; AAM10776.1; SEQUENCE 127 AA; 14317 vm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AX4
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NCBI_TaxID=44689;
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2 (NTF2) from.
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ahmann R., Baumgart C., Pa
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                                                                                                                                                                                                                    12 ---GlyLysGlnPheValGluHisTyrTyrGlyIlePheAspSerAsnArgAlaGlyLeu
                                                                                                                                                                                       TCCCGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAA
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                                                                                                                                                                                                                                                                                                           TCCATAGAACCAGAGATGGCATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGA
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                                                                                                                               GAATCCTTGAGTGAGTTTTTTGAAATGTTGCCT----TCCAGCGAGTTCCAAATCAGC
                                                                                                                                                           ThrGlnIleTyrGlnGlnGlnThrThrLeuThrTrpGluGlyLysPheLeuSerGlyAla
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               GTCATCTGTGGATCAGTGAAGTTTGAGGGGAACAAACAACGGGACTTCAACCAG----AAC
                                          SerIleAspCysGlnGlnThrTyr
                                                                     GTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTT
                                                                                                  AspAlaIleValLysHisIleValGluLeuProPheGlnGlnThrAsnArgLysIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ThrProSerPheProGlyGlyIleLeuValPheValSerGlyAsnLeuGlnLe
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AAM10776.1; -.
AA; 14317 MW; 2D45B1B20021B2
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129.00
46.48%
23.24%
8.66%
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rra G., April J
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Last annotation updat
factor similar to nucl
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of Dictyostelium.";
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01-OCT-2000
01-OCT-2000
01-JUN-2002
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SEQUENCE FROM N.A.

Cordero Otero R.R., Lepingle A., Gaillardin C.

"RPH1 gene from Yarrowia lipolytica.";

"RPH1 --1 , wav-2000) to the EMBL/GenBank/DDBJ
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Submitted (APR-2000) to the EMI
EMBL; AF260231; AAF70316.1; -.
HSSP: P13662; 100N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi, Ascomycota; Saccharomycotina;
Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
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CCCAGCAACACAGTGTGGGAAGATCGCAAGTGACTGCTTCCGC
                                                                                                                  CATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAG
                                                                                                                                             ValGlyLeuProPheGlyGlnValArgHisLysIleSerAspIleAspAlaGlnPro---
                                                                                                                                                                                                       SerMetLeuThrPheThrGlyThrGlnHisGlnGlyAlaGlnAlaIleValGluLysLeu
                                                                                                                                                                                                                                  SerValAspPheAsnThrLeuAlaLysGlnPheCys------GluPhe-----
                                                      TTTGAGGGGAACAAACAACGGGACTTCAACCAGAACTTCATCCTGACCGCCCAGGCCTCA
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Q917J5;
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01-JUN-2002
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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RIN OR CG9412.
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Amanatides P.G.,
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RRM; 1.
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.E., Li P.W.,
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S., Ashburner M., H
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01-OCT-2000
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                                                                                                                                                                                                                                                                                       MEDLINE-20191744; PubMed-10725247; Pagman C., Mayes C.A., Fanto M., Haynes S.R., Mlodzik M.; Pagman C., Moscophila homolog of the RasGAP SH3 binding functions in Ras and Rho mediated signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                         PROSITE; PS50102; SEQUENCE 690 AA
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                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drosophilidae; NCBI_TaxID=7227;
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                                                                                                                                                       SMART; SM00360; RRM;
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EMBL; AF231031; AAF68949.1; -
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                          A Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Heiman T.J., Weel M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., M.Cherry C. Morberson D.,
Acchara M. M. Macharry C. Morberson D.,
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01-JUN-2002
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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RIN OR CG9412.
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EMBL; AY058617; AAL13846.1; --
ETyBase; FBgn0015778; rin.
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Palazzolo
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M., Pittman G.S., Pan S., Pollard J., Purl V., Reese
, Remington K., Saunders R.D.C., Scheeker F., Shen H
, Siden-Klamos I., Simpson M., Skupski M.P., Smith T.

Spradling A.C., Stapleton M., Strong R., Sun E.,
R., Tector C., Turner R., Venter E., Wang A.H., Wang
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cleb J., Paragas V., Park S.,
S.E., Rubin G.M., Celniker S
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Dorsett V., Farfan D., Frise E., Gec
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Q96VN3;
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HSSP; P13662; 10UN
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Espaso E.A., Penalva M.A.;
"Nuclear transport factor 2 f.
"Nuclear transport factor 1.
EMBL; AY038983; AAK71467.1;
InterPro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
SEQUENCE 125 AA; 13871 MW;
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01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                        Q21351
Q21351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Nuclear transport factor 2.
                                                                           Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eurotiales; Trichocomaceae;
 Submitted (JAN-1996)
                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5072;
                                                                                                                                               K08F4.2
                                                                                                                                                       K08F4.2 protein.
                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                      CGC 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyIleIleGluLysLeuThrSerLeuProPheGlnLysValGlnH1sGlnValSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTTGAGTGAGTTTTTTGAAATGTTGCCT----TCCAGCGAGTTCCAAATCAGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProLeuTyrArgAspHisSerMetLeuThrPheGluThrSerAlaIleGlnGlyValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCCTGTACATGGGCACAGCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                   ATCCTGACCGCCCAGGCCTCACCCAGCAACACAGTGTGGGAAGATCGCAAGTGACTGCTTC 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTGTGGATCAGTGAAGTTTGAGGGGAACAAACAA----CGGGACTTCAACCAGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAspAlaGlnProSerGlyGluHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACCACGGTCCTTGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaGlnGlnPhevalThrPheTyrTyrGlnThrPheAspGlyAsnArgAlaGlyLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                 ValThrGlyAlaLeuLeuValAspGluGluLysAsnProMetAsnTyrThrGlnThrPhe
                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                           PRELIMINARY;
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112.50
47.11%
.27.27%
7.56%
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                                                                                                       Nematoda;
                to the
                                                                                                                                                                           01,
21,
                                                                                              oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Aspergillus nidulans.";
EMBL/GenBank/DDBJ databases.
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Last sequence up
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-GlyIleLeuValLeu

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RESULT 12
Q9VJ85
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Investigating blorby: (1998). Science 282:2012-2018(1998). Science 268879; CAA93082.1; -. 268879; CAA93082.1; -.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A.,
Amanatides P.G., Scherer S.E., Li P.W.
                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                     Q9VJ85;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                       CG10174 protein.
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                                              SEQUENCE FROM N.A.
                                                                                                                 Drosophila melanogaster (Fruit fly)
                                                                                                                                CG10174
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                                                                   NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                           ValIleIleAsnValIleGlyThrValAsnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt ArgLysAlaIleThrLysPheTyrGlyHisGluSerLysPheTyrLeuAspAspGlnValue} \\
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Conservative:
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Indels:
Gaps:
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  Evans C.A., Goc., Hoskins R.A.,
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                                                                                                       Hexapoda;
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                                                                                            Brachycera;
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            Gocayne
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez JR., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Liu X., Mattei B., Kolira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Staplecon M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Sibes B.R., Myers E.W., Rubin G.M., Venter J.C.,
RA Sibes B.R., Myers E.W., Rubin G.M., Venter J.C.,
RT Tengence 287:2185-2195/2000.
DR HSSP, P13662; 100N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P13662; ICC...
F1yBase; FBgn0032680; CGIO-
F1yBase; FBgn002075; NTF2.
IFR002075; NTF2.
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Beeson K.Y., Benos P.V., Berman B.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sutton G.G., Wortman J.R., Yan Brandon R.C., Rogers Y.-H.C.,
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Sutton G.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 GAGGAGTTTGTCAATGTCTACTACACCACCATGGAT-----AAGCGGCGCGTTTGCTG
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84
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                                                  CAAGAATCCTTGAGTGAGTTTTTTGAAATGTTGCCTTCCAGCGAGTTCCAA---
                                                                                                                                                                                                                                                                                                                                                                                              TCCCGCCTGTACATGGGCACA---GCCACCCTGGTCTGGAATGGCAATGCTGTTTCAGGA
                                                                                                          ArgValIleThrThrValAspSerGlnProThrSerAspGlyGly-
                                                                                                                                                                                                                           AlaProLysile:
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·ValLeuIleIleValLeuGlyArgLeuLysCysAspAspAspProProHisAlaPhe
                                                                                                                                           ----ATCAGCGTGGTAGACTGCCAGCCTGTTCATGATGAAGCCACACCAAGCCAGACC
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V., Berman B.P., Bhandari D., Bolshakov S.,
.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG10174
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                                                                                                                                                                                                                        LeuGluLysValGlnSerLeuSerPheGlnLysIleAla
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Mismatches:
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Smith H.O.,
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s G.L.G.,
'in D.,
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Pfam; PF00442; UCH-1;
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    AACCAGAACTTCATCCTGACCGCCCAGGCCTCACCCAGCAACACGTGTGGAAGATCGCA 496
                                                                               -- LysProAsnGlyGlySerLeuPheValAla 118
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafil H., Bei B., Chin C., Chlou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) F17L21.10 (Similar to nuclear transport factor 2).
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                          122 AA
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                                                                           103 SerGlnIlePheLeuLeu---
                                                                                                                                                                                                                                      HisAspilePheArg 123
                                                                                                                                                           497 AGTGACTGCTTCCGC 511
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Submitted (DEC-1998)
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Submitted (APR-1998)
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437
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TCCTTGAGTGAGTTTTTTGAAATGTTGCCT-----TCCAGCGAGTTCCAAATCAGCGTG 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 AsnileValAlaLysLeuThrGlyLeuProPheGlnGlnCysLysHisAsnileThrThr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGAGGAGTTTGTCAATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCĊ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 ATCCTGACCCCCAGGCCTCACCCAGCAACACAGTGGAAGATCGCAAGTGACTGCTTC
    L)
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Cheuk R:, Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.K., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AQ04557; AAF99749.1;
EMBL; AY042889; AAK6889.1;
EMBL; AY072473; AAL66888.1;
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333
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124
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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Amerik A., Li S.-J., Hochstrasser M.;
"Analysis of the deubiquitinating enzymes
                                                                                                                                                                                                                                                                                                                                                                                          Indels:
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InterPro; IPR001763; Rhodanese-like
InterPro; IPR001394; UCH-2.
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                                                                                                                                                                                                                                     13527 MW;
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SEQUENCE 122 AA;
                                                                                                                                                                       P13662; 10UN.
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Best Local Similarity:
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SMART;
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spCysPheLysGluPheThrLysLeuGluThrLeuGluLysAspGluLeuTrpTyrCysP
                                                                                                                       TGCCGAGGTTGAACTCTTTTTTGTTGCTCAAGTTCTAGGAGTCCCTTTCCTGAATATATA 720
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Page N.M., Butlin D.J., Manyonda I., Bicknell Submitted (FEB-1998) to the EMBL/GenBank/DDBJ EMBL; AF050199; AAC05749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07,
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Mammalia; Eutheria;
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                                                                                                                 CCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTGAGGGGAACAACAACGGGACT
                                                                                                                                                                                 LeuSerTrpHisGlnCysLeuLeuIleProPro---
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Catarrhini; Hominidae; Homo
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	Search completed: June 24, 2003, 19:36:51
	Db 175CysCysCysSerSerIleGluThrArgGlyProArg 186
	OY 615 ACACAAGTICATITCTGTTGCGGAGACACTGCAGACTCCACTGTGCCGAGG 668
174	Db 173 1
514	OY 555 GCTTCATTCAGCCCTAGCTCTGTAGAGAAATGCAAACCTCGACTCTCAAGGATGTGAGGA 614
172	Db 160 AlaAlaGluAlaAlaAlaAlaArgLeuGlySerSerser
554	QY 495 CAAGTGACTGCTTCCGCTTCCAGGACTGGGCCAGCTAGTGGGGGGTGGCAGAGGTCTCTTT 554

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Result
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Maximum Match 100%
Listing first 45 summaries
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Sequence 346, App	Sequence 210, App	Sequence 99, Appl		 Sequence 1637, Ap 	Sequence 1962, Ap		Sequence 1962, Ap	Sequence 1636, Ap	-	Sequence 6283, Ap	1961, 7	Sequence 1638, Ap	e 1963,		Sequence 1963, Ap	Sequence 54, Appl	Sequence 10222, A	Sequence 610, App	Sequence 6305, Ap	Sequence 115, App	19	Sequence 3, Appl1	Sequence 85, Appl	Sequence 1, Appli

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SEQ ID NO 393
LENGTH: 1387
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CURRENT FILING DATE: 2001-01-17
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OTHER INFORMATION: n
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ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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es 978; Conservative
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                                                                                                               Sequence 1682, Application Patent No. US20020132753A1 GENERAL INFORMATION: APPLICANT: Rosen et al.
              SOFTWARE: PatentIn Ver.
SEQ ID NO 1682
LENGTH: 8918
                                                                               TITLE OF INVENTION: Nucleic FILE REFERENCE: PTZ23
CURRENT APPLICATION
                                             CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1792
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Sequence 1683, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PAI NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                    RESULT 4
US-09-796-692-8289
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Sequence 8289, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
LENGTH:
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Best Local Similarity
Matches 749; Conserv
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ORGANISM: Homo sapiens
-09-764-864-1683
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                 AND
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; TYPE: DNA
; ORGANISM: HOMO:
US-09-796-692-8289
 RESULT 5
US-10-040-862-8289
; Sequence 8289, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
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                                                                                                                                            TAGTAAAACACGTTGCCTGTTTTCAGTTAACACTGGTAATGCCATTTTAATATATGGCTT 1028
                                                                                                                                                                                            CTCACTGTGAACCCAGCCTATTGCAAAAATAAAATCTTTTATAATATTATCTATGGGAT
TGGAATTGCATATAGAGATGTTCAGTGGTCGTTTTTCATTTTAAGTAATTTTTTGTTTT 1146
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Q for Windows Version
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Pred. No. 2.1e-96;
0; Mismatches 2;
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240 968 120 848 788

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; ORGANISM: HOMO
US-10-040-862-8289
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Best Local Similarity 99.5

Conservative
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URRENT FILING DATE: 2001-11-06
RIOR APPLICATION NUMBER: US 60/186,126
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APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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FILING DATE: 2000-05-01
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PLICATION NUMBER: US 60/223,378
LING DATE: 2000-08-07
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                                                                                                                                                                                                                                                                                                  CTCACTGTGAACCCAGCCTATTGCAAAAATAAATCTTTTTATAATATTATCTATGGGAT 908
                                                                                                                                                                                                                                                                                                                                                                               TACATTCCACTAATGACATTCTTATAATAATAATTAAACACATGATCTTGGTACTAACATA 848
TGGAATTGCATATAGAGATGTTCAGTGGTCGTTTTTCATTTTAAGTAATTTTTTGTTTT 1146
                                                        TTTCAAATCAGTTCAGTGAAAATAGTACAGATTTAGGTTTACATAACTACTCTGACATAC 1088
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IG DATE: 2000-04-27
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99.5%;
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Pred. No. 2.1e
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US-09-764-864-394
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                                     ATGAAGCCACCAAGCCAGACCACGGTCCTTGTTGTCATCTGTGGATCAGTGAAGTTTG
                                                              AGCAAGCAACTCAGTCCCAAACTACAGTTCTTGTTGTGACCAGTGGAACTGTGAAGTTTG 461
                                                                                                            TTGAAATGTTGCCTTCCAGCGAGTTCCAAATCAGCGTGGTAGACTGCCAGCCTGTTCATG
                                                                                                                                 TTGACACATTGCCTTCTAGTGAGTTCCAGGTCAATATGTTAGATTGCCAACCAGTTCATG
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Sequence 394, Application US/09764864 Patent No. US20020132753A1
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                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                  162 CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGGTGAGGAGTTTGTCA 221
282 AGGCCACCTTAATATGGAATGGAAATGCTGTTTCAGGGCTGGATGCCCTAAATAATTTTT
                                                                               222 ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA
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US-09-796-692-4160
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                                              Sequence 4160, Application US/09796692 Publication No. US20020198362A1
                                  GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-3-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER.
FILE REFERENCE: 210121.504
      APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A
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APPLICANT: Xu, Jiangchun
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LOCATION: (1)...(318)
OTHER INFORMATION: n = A,T,C
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: Pred. No. 1.6e
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RESULT 9
US-10-040-862-4160
; Sequence 4160, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
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; ORGANISM: Homo sapiens US-09-796-692-4160
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SEQ ID NO 4160
LENGTH: 318
TYPE: DNA
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/190,479 PRIOR FILING DATE: 2000-03-17
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PRIOR FILING DATE: 2000-03-01
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CURRENT FILING DATE: 2001-03-01
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PRIOR FILING DATE: 2000-08-07
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nes 234; Conserv
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                         TCCTGCTGACTGCTCAG 511
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Pred. No. 2.2e-37;
0; Mismatches 83
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; ORGANISM: Homo sapiens
US-10-040-862-4160
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4160
LENGTH: 318
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URRENT FILING DATE: 2001-11-06
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(TILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
(TILE OF INVENTION: Hematological Malignancies
(ILE REFERENCE: 014058-013520US
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APPLICATION NUMBER: US 60/200,545
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                                                                                                                                                                                          ATATGTTAGATIGCCAACCAGTTCATGAGCAAGCAACTCAGTCCCAAACTACAGTTCTTG 434
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                                TCATCCTGACCGCCCAG 317
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                                                                 TCCTGCTGACTGCTCAG 511
                                                                                                    CATION NUMBER: US 60/223,378 US DATE: 2000-08-07 CATION NUMBER: US 09/796,692
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ilarity 73.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TE: 2000-07-14
ON NUMBER: US 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON NUMBER: US 60/200,999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER: US 60/223,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US 60/218,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US 60/206,201: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 184.2; DB 9
Pred. No. 2.2e-37;
0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
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                                                                                                                                 Query Match
Best Local S
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6557
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                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                            ENGTH: 417
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222 ATATTTACTATGAGACAATGGATAAAAGAAGAGG 255
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RESULT 10

ATGTCTACTACACCACCATGGATAAGCGGCGCG

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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n = A,T,C or
US-09-918-995-6557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2901, Application US/09918995 Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF CONTROL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 38054
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PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                              162 CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 ATGTCTACTACACCACCATGGATAAGCGGCGGCGTTTGCTGTCCCGCCTGTACATGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 CGTCTCTGGATTTTAAAACTTATGTAGATCAGGCATGTAGAGCTGCTGAGGAGTTTGTCA
315 CATCTGTGGATTTCAAGACCTATGTGGATCAGGCCTGCAGAGCTGCTGAGGAGTTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 CAGCCACCCTGGTCTGGAATGGCAATG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 ATATTTACTATGAGACAATGGATAAAAGAAGACGGGCACTAACCAGGCTGTATCTGGACA
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                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Application US/09918995
5. US20030073623A1
                                                                                                                                                                                                5.4%;
ilarity 78.7%;
Conservative
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                                                                                                                                                                                           ; Score 62; DB
; Pred. No. 5.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                        Length 417
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US-10-239-676-96
                                                                                                 RESULT 13
US-10-239-676-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                        GENERAL
                                                         sequence 90, Application US/10239676 Publication No. US20030082609A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-09-01
NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/EP01/03968
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICANT: BERLIN, Kurt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4546 GAATARAAGATATATTTATTGAAATATTAAATAAGAGAGTAGAGTTTGTTATATTAGGA 4605
                                                                                                                                                                                      4786 TAATAGTAAGAGATTTTAATGTTTTATTTTT
                                                                                                                                                                                                                                                                                                           1054 TACAGATTTAGGTTTACATAACTACTCTGACATACTGGAATTGCATATAGAGATGTTCAG 1113
                                      INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                            994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814 AATAATATTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCCAGCCTATTGCA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754 AAGAGCTTTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTAT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/239,676 FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                            TGGTCGTTTTTCATTTTAAGTAATTTTTTTT 1144
                                                                                                                                                                                                                                                                                                                                                                                          GTTAACACTGGTAATGCCATTTTAATATGGCTTTTTCAAATCAGTTCAGTGAAAATAG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAGTGGAGTTTTTTGGTTATTAGGTTAATTTTCTAGTAAAACACGTTGCCTGTTTTTCA 993
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                                                                                                                                                                                                                                                                                                                                                   GTTAAAAAGGTTAGTTTATTTAGAAGATATGATAATTAGAAAATATATATGTATAAAAATAT 4725
PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10239676
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Pred. No. 2
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Sequence 209, Appli Publication No. US2 GENERAL INFORMATION

Application US/10239676
o. US20030082609A1

APPLICANT: OLEK,

APPLICANT:

PIEPENBROCK, Christian

Alexander

TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation

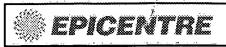
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RESULT 14
US-10-239-676-209
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; LOCATION: (1818, 1930..1931,
US-10-239-676-90
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/239,676
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                                                                   AACACATGATCTTGGTACTAACATACTCACTGTGAACCCAGCCTATTGCAAAAAATAAAAT 883
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Pred. No. 1.8;
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-209
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S-10-172-086-18/c
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Best Local Similarity 45.6
Matches .187; Conservative
                                                                                                 CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 18
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Epigenomics AG
                                                                                                                                                                                                                                                                                Sequence 18, Ap
Publication No.
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CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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    OTHER INFORMATION:
                                                                            ENGTH:
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vo. US20030113750A1
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                                                                                                                                                                                                   Method and nucleic acids for the differentiation of prostate tumors
chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
17262 ATTATATATACAATAACAATTA 17241
                                                                    17322 ТАТТАВАВАВАСАВАВАВАВАВАВТТТТАВТСАСАСТАВВАССАВВАТТТАВАВАВАТАВВЯ 17263
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                                                                                                        821
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                                    881
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                                 AATCTTTTTATAATATTATCTA
                                                                                                       TTAAACACATGATCTTGGTACTAACATACTCACTGTGAACCCCAGCCTATTGCAAAAATAA 880
                                                                                                                                                              TTAAAACTATTTTTTTACATGCCTTATATACATTCCACTAATGACATTCTTATAATAATA 820
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47.78;
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Pred. No. 4
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                                    902
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Search completed: June 28, 2003, 03:41:59 Job time : 191.807 secs





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ARTICLES

Normalization and subtraction: two approaches to facilitate gene discovery

MF Bonaldo, G Lennon and MB Soares

Department of Psychiatry, College of Physicians and Surgeons of Columbia University, New York, New York, USA

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Large-scale sequencing of cDNAs randomly picked from libraries has proven to be a very powerful approach to discover (putatively) expressed sequences that, in turn, once mapped, may greatly expedite the process involved in the identification and cloning of human disease genes. However, the integrity of the data and the pace at which novel sequences can be identified depends to a great extent on the cDNA libraries that are used. Because altogether, in a typical cell, the mRNAs of the prevalent and intermediate frequency classes comprise as much as 50-65% of the total mRNA mass, but represent no more than 1000-2000 different mRNAs, redundant identification of mRNAs of these two frequency classes is destined to become overwhelming relatively early in any such random gene discovery programs, thus seriously compromising their cost-effectiveness. With the goal of facilitating such efforts, previously we developed a method to construct directionally cloned normalized cDNA libraries and applied it to generate infant brain (INIB) and fetal liver/spleen (INFLS) libraries, from which a total of 45,192 and 86,088 expressed sequence tags, respectively, have been derived. While improving the representation of the longest cDNAs in our libraries, we developed three additional methods to normalize cDNA libraries and generated over 35 libraries, most of which have been contributed to our integrated Molecular Analysis of Genomes and Their Expression (IMAGE) Consortium and thus distributed widely and used for sequencing and mapping. In an attempt to facilitate the process of gene discovery further, we have also developed a subtractive hybridization approach designed specifically to eliminate (or reduce significantly the representation of) large pools of arrayed and (mostly) sequenced clones from normalized libraries yet to be (or just partly) surveyed. Here we present a detailed description and a comparative analysis of four methods that we developed and used to generate normalize cDNA libraries from human (15), mouse (3), rat (2), as well as the parasite Schistosoma mansoni (1). In addition, we describe the construction and preliminary characterization of a subtracted liver/spleen library (INFLS-SI) that resulted from the elimination (or reduction of representation) of -5000 INFLS-IMAGE clones from the INFLS library.

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Display	default	Show: 20	Send	file File	<u>.</u>	, · ·		

1: AW274482. xv30c09.x1 Soares...[gi:6661512]

Links

IDENTIFIERS

dbEST Id:

3657583

EST name:

xv30c09.x1

GenBank Acc:

AW274482

GenBank gi:

6661512

CLONE INFO

Clone Id:

IMAGE: 2814640 (3')

Source:

NCI

DNA type:

cDNA

PRIMERS

Sequencing:

-40UP from Gibco

PolyA Tail: Unknown

SEQUENCE

CAGACTCCTCAGCAGCTCTGCAGGCCTGATC

Quality:

High quality sequence stops at base: 466

Entry Created:

Jan 3 2000

Last Updated:

Jan 3 2000

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ($\underline{info@image.llnl.gov}$) for further

information.

PUTATIVE ID

Assigned by submitter WP:Y71F9A 279.B CE22843;

LIBRARY

Lib Name:

Soares_NFL_T_GBC_S1

Organism:

Homo sapiens

Organ:

pooled

Lab host:

DH10B

Vector:

pT7T3D-Pac (Pharmacia) with a modified polylinker

h cb hg e e e fcg c e e e b c e e

R. Site 1:

Not I

R. Site 2:

Eco RI

Description:

Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction

by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: E-mail: Robert Strausberg, Ph.D.

cgapbs-r@mail.nih.gov

CITATIONS

Title:

National Cancer Institute, Cancer Genome Anatomy Project

(CGAP), Tumor Gene Index

Authors:

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap

Year:

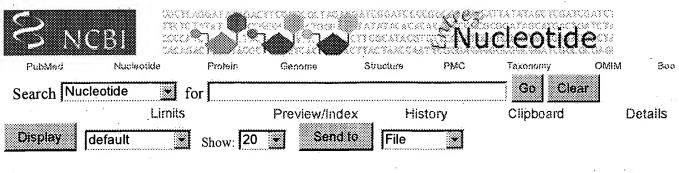
Status:

Unpublished

MAP DATA

<u>Disclaimer</u> | Write to the Help Desk NCBI | NLM | NIH

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1: BF195575. 7n85b11.x1 NCI_CG...[gi:11082605]

Links

IDENTIFIERS

dbEST Id:

6660525

EST name:

7n85b11.x1

GenBank Acc:

BF195575

GenBank gi:

11082605

CLONE INFO

Clone Id:

IMAGE: 3571173 (3')

Source:

NCI

DNA type:

cDNA

PRIMERS

PolyA Tail:

Unknown

SEQUENCE

Quality:

High quality sequence stops at base: 466

Entry Created:

Nov 3 2000

Last Updated:

Nov 3 2000

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library

Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by:

Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send

email to: info@image.llnl.gov

PUTATIVE ID

Assigned by submitter

TR:Q9UKK6 Q9UKK6 NTF2-RELATED EXPORT PROTEIN NXT1.;

LIBRARY

h cb hg e e e fcg c e e e b c e e

Lib Name:

NCI_CGAP_Ov18

Organism:

Homo sapiens

Organ:

ovary

Tissue type:

fibrotheoma

Lab host:

DH10B (phage-resistant)

Vector:

pT7T3D-Pac (Pharmacia) with a modified polylinker

R. Site 1: R. Site 2:

Not I Eco RI

Description:

Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: E-mail: Robert Strausberg, Ph.D. cgapbs-r@mail.nih.gov

CITATIONS

Title:

National Cancer Institute, Cancer Genome Anatomy Project

(CGAP), Tumor Gene Index

Authors:

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap

Year:

Status:

Unpublished

1997

MAP DATA

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Jul 30 2003 12:44:50